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152519

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Scientific and Technical Information Center

SEARCH REQUEST FORM

Requester's Full Name: JANE ZARA Examiner #: 77512 Date: 5-4-05
Art Unit: 1635 Phone Number: 2-0765 Serial Number: 091340-595
Location (Bldg/Room#): 2D28 (Mailbox #): 2-18 Results Format Preferred (circle): PAPER DISK

To ensure an efficient and quality search, please attach a copy of the cover sheet, claims, and abstract or fill out the following:

Title of Invention: Compos + methods for Tumor Therapy

Inventors (please provide full names): POHARJER et al

Earliest Priority Date: 6-28-99

Search Topic:

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc., if known.

For Sequence Searches Only Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

MEJ

Please search Seq ID No: 1

NA 2133 For interference + regular data
loss.

No size limits. Zar 595
5/6 5p

01 Thanks.

STAFF USE ONLY

Type of Search

Vendors and cost where applicable

Searcher: _____ NA Sequence (#) _____

_____ STN _____ Dialog

Searcher Phone #: _____ AA Sequence (#) _____

_____ Questel/Orbit _____ Lexis/Nexis

Searcher Location: _____ Structure (#) _____

_____ Westlaw _____ WWW/Internet

Date Searcher Picked Up: _____ Bibliographic _____

_____ In-house sequence systems

Date Completed: _____ Litigation _____

_____ Commercial _____ Oligomer _____ Score/Length
_____ Interference _____ SPDI _____ Encode/Transl
_____ Other (specify)

Searcher Prep & Review Time: _____ Fulltext _____

Online Time: _____ Other _____

Result No.	Query			Length	DB	ID	Description
	Score	Match					
1	1000.2	46.9	2079	3	53	09-297-751-1	Sequence 1, Appli
2	928.2	43.5	933	6	53	40934-12	Patent No. 5340934
3	928.2	43.5	933	6	53	40934-12	Patent No. 5340934
4	831.6	39.0	7375	3	US-09-513-442-1		Sequence 1, Appli
5	713.6	33.5	844	4	US-10-000-489-19		Sequence 19, Appl
6	469	22.0	481	4	US-09-640-173-190		Sequence 190, App
7	469	22.0	481	4	US-09-713-550-190		Sequence 190, App
8	469	22.0	481	4	US-09-825-294-190		Sequence 190, App
9	469	22.0	481	4	US-09-970-966-190		Sequence 189, App
10	450.4	21.1	460	4	US-09-640-173-189		Sequence 189, App
11	450.4	21.1	460	4	US-09-713-550-189		Sequence 189, App
12	450.4	21.1	460	4	US-09-825-294-189		Sequence 189, App
13	450.4	21.1	460	4	US-09-970-966-189		Sequence 189, App
14	428.4	20.1	490	4	US-09-513-998C-141		Sequence 141, App
C 15	407.8	19.1	454	3	US-09-404-879A-179		Sequence 179, App
C 16	407.8	19.1	454	4	US-09-338-933-179		Sequence 179, App
C 17	407.8	19.1	454	4	US-09-215-681-179		Sequence 179, App
C 18	407.8	19.1	454	4	US-09-216-003A-179		Sequence 179, App
C 19	407.8	19.1	454	4	US-09-667-857-179		Sequence 179, App
20	406	19.0	454	3	US-09-404-879A-180		Sequence 180, App
21	406	19.0	454	4	US-09-338-933-180		Sequence 180, App
22	406	19.0	454	4	US-09-215-681-180		Sequence 180, App
23	406	19.0	454	4	US-09-216-003A-180		Sequence 180, App
24	406	19.0	454	4	US-09-667-857-180		Sequence 180, App
25	401	18.8	401	4	US-09-702-705-1034		Sequence 1034, Ap
26	401	18.8	401	4	US-09-736-457-1034		Sequence 1034, Ap
27	401	18.8	401	4	US-09-614-124B-1034		Sequence 1034, Ap


```

; APPLICANT: TERMINE, JOHN D.; YOUNG, MARIAN F.; FISHER, LARRY W.
;
; ROBEY, PAMELA G.
;
; TITLE OF INVENTION: CDNA SEQUENCES OF HUMAN BONE MATRIX PROTEINS
;
; NUMBER OF SEQUENCES: 13
;
; CURRENT APPLICATION DATA:
;
; APPLICATION NUMBER: US/07/432,044
;
; FILING DATE: 03-NOV-1989
;
; SEQ ID NO:12:
;
; LENGTH: 933
;
S340934-12

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Query Match	43.5%	Score 928.2	DB 6	Length 933
Best Local Similarity	99.7%	Pred. No. 1.1e-236		
Matches 930	Conservative 0	Mismatches 3	Indels 0	Gaps 0

Qy	37	CCACTGAGGGTTCCACGACCACCATGAGGGCCTGGATCTTCTTTCTTCCTTTGCTGCTGCGCGGG	96
Db	1	CCACTAAGGGTTCCAGCACCATGAGGGCCTGGATCTTCTTTCTTCCTTTGCTGCTGCGCGGG	60
Qy	97	AGGCGCTTGGCAGCCCTTCAGCAAGAAAGCCCTGCCTGATGAGACAGAGGTGGTGAAGAA	156
Db	61	AGGCGCTTGGCAGCCCTTCAGCAAGAAAGCCCTGCCTGATGAGACAGAGGTGGTGAAGAA	120
Qy	157	ACTGTGCGAGGTCATGAGGTATCTGTGGAGCTAATCTGTCCAGTGAATCTGTGCTGGAAGT	216
Db	121	ACTGTGCGAGGTCATGAGGTATCTGTGGAGCTAATCTGTCTCAGGTGGAAGT	180
Qy	217	GAATTTGATGATGTGTGAGAGAAACCGAAGAGGAGTGGTGGCGGAAATCCCTGCGCAG	276
Db	181	GAATTTGATGATGTGTGAGAGAAACCGAAGAGGAGTGGTGGCGGAAATCCCTGCGCAG	240
Qy	277	AACCAACACTGCAAAACHCGGCAAGGTGTGCGAGCTGAGTGAATGAGAACACACCCCATGTGC	336
Db	241	AACCAACACTGCAAAACHCGGCAAGGTGTGCGAGCTGAGTGAATGAGAACACACCCCATGTGC	300
Qy	337	GTGTGCGCAGGACCCACACAGCTGCCAGCCCCCATGCGCAGTTTGAGAGGTTGTGCAGC	396
Db	301	GTGTGCGCAGGACCCACACAGCTGCCAGCCCCCATGCGCAGTTTGAGAGGTTGTGCAGC	360
Qy	397	AATGACAAACAGACCTTTCGACTCTTCTCGCCACTCTTTTGGCCACAAAGTGCACCCCTGGAG	456
Db	361	AATGACAAACAGACCTTTCGACTCTTCTCGCCACTCTTTTGGCCACAAAGTGCACCCCTGGAG	420
Qy	457	GGCAACCAAGAGGGGCAACAGCTCCACTGAGCTACATCGGGCCTTGGAAATACATCCCC	516
Db	421	GGCAACCAAGAGGGGCAACAGCTCCACTGAGCTACATCGGGCCTTGGAAATACATCCCC	480
Qy	517	CTTTGCTCGACTCTGAGCTGACCGAATCTCCCTCGCGCATGCGGGACTGGCTCAAGAAC	576
Db	481	CTTTGCTCGACTCTGAGCTGACTGAATTTCCCTCTCGCATGCGGGACTGGCTCAAGAAC	540
Qy	577	GTCTGTGTACCTTGATGAGGGATGAGGACAAACCTTTCTGACTGAGAAGCAGAAG	636
Db	541	GTCTGTGTACCTTGATGAGGGATGAGGACAAACCTTTCTGACTGAGAAGCAGAAG	600
Qy	637	CTGGGGTGAAGATCCATGAAATGAGAGCGCTTGGAGGACAGGACCAACCCCGTG	696
Db	601	CTGGGGTGAAGAAAGATCCATGAAATGAGAAAGCGCTTGGAGGACAGGACCAACCCCGTG	660
Qy	697	GAGCTGTGCGCCGGGACTTCGAGAGAACTATAACATGTACATCTTCCCTGTACACTGG	756
Db	661	GAGCTGTGCGCCGGGACTTCGAGAGAACTATAACATGTACATCTTCCCTGTACACTGG	720
Qy	757	CAGTTGGGCAGCTGGACAGACCCCATTTGACGGGTACCTCTCCCAACCGAGCTGGCT	816
Db	721	CAGTTGGGCAGCTGGACAGACCCCATTTGACGGGTACCTCTCCCAACCGAGCTGGCT	780
Qy	817	CCACTGGTGTCTCCCTCATCCCATGGACATTGCACACCCCGCTTTTTCGAGACCTGT	876
Db	781	CCACTGGTGTCTCCCTCATCCCATGGAGCATTTGCACACCCCGCTTTTTCGAGACCTGT	840
Qy	877	GACCTGGAACAATGACAAAGTACATCGCCCTGAGTGAAGTGGGCGGCTGCTTGGCATCAAG	936

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Db      841  GACCTGCACANTGACAAAGTACATCGCCCTGGATGATGCGGCGGCTGCTTCGCGCATCAAG  900
Qy      937  CAGAAGGATATCGACAAGGATCTTTGTGATCTAA  969
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Db      901  CAGAAGGATATCGACAAGGATCTTTGTGATCTAA  933
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RESULT 3
5340934-12
; Patent No. 5340934
; APPLICANT: TERMEINE, JOHN D.; YOUNG, MARIAN F.; FISHER, LARRY W.
; ROBEY, PAMELA G.
; TITLE OF INVENTION: CDNA SEQUENCES OF HUMAN BONE MATRIX PROTEINS
; NUMBER OF SEQUENCES: 13
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/432,044
; FILING DATE: 03-NOV-1989
; SEQ ID NO:12:
; LENGTH: 933
5340934-12

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Query Match	43.5%	Score 928.2	DB 6	Length 933
Best Local Similarity	99.7%	Pred. No. 1.1e-236		
Matches 930	Conservative 0	Mismatches 3	Indels 0	Gaps 0
Qy	37	CCACTGAGGGTTCCACGACACATCAGGGCCCTGGATCTCTTCTCTCTCTGCTGCTGCGCGG	96	
Db	1	CCACTAAGGGTTCCAGACACATCAGGGCCCTGGATCTCTTCTCTCTTCTCTGCTGCGCGG	60	
Qy	97	AGGGCCCTTGGCAGCCCTTCAGCAAGAAGCCCTGCCTGATGAGACAGAGTGTGGAAGAA	156	
Db	61	AGGGCCCTTGGCAGCCCTTCAGCAAGAAGCCCTGCCTGATGAGACAGAGTGTGGAAGAA	120	
Qy	157	ACTGTGCGCAGAGTGACTGAGGTATCTGTGGAGGCTAATCTCTGTCCAGGTGGAAGTAGGA	215	
Db	121	ACTGTGCGCAGAGTGACTGAGGTATCTGTGGAGGCTAATCTCTGTCCAGGTGGAAGTAGGA	180	
Qy	217	GAATTTGATGATGTTGCAGAGGAACCGAACAGAGAGGTGTGGCGGAAATCCCTGCCAG	276	
Db	181	GAATTTGATGATGTTGCAGAGGAACCGAACAGAGAGGTGTGGCGGAAATCCCTGCCAG	240	
Qy	277	AACCCACCACTGCRAACCGGCAAGGTGTGCGAGCTGGAATGAGAAACAAACCCCCATGTGC	336	
Db	241	AACCCACCACTGCRAACCGGCAAGGTGTGCGAGCTGGAATGAGAAACAAACCCCCATGTGC	300	
Qy	337	GTGTGCCAGACCCCAACAGCTGCCAGCCCCCATTTGGCGAGTTTGAGAGGTGTGCAGC	396	
Db	301	GTGTGCCAGACCCCAACAGCTGCCAGCCCCCATTTGGCGAGTTTGAGAGGTGTGCAGC	360	
Qy	397	AATGACAAACAGACCTTCGACTCTTCCTGCCACTCTTCCTGCCACAAAGTGACACCTGGAG	456	
Db	361	AATGACAAACAGACCTTCGACTCTTCCTGCCACTCTTCCTGCCACAAAGTGACACCTGGAG	420	
Qy	457	GGCACCAAGAGGGCCCAACAGCTCCACCTGACACTACATCGGGCCCTTGCAATACATCCCC	516	
Db	421	GGCACCAAGAGGGCCCAACAGCTCCACCTGACACTACATCGGGCCCTTGCAATACATCCCC	480	
Qy	517	CCTTGCCTGGAACCTTGAGTGACCGGAATTCCTCCCTGCGCATCGGGGACTGGCTCAAGAC	576	
Db	481	CCTTGCCTGGAACCTTGAGTGAGTAAATCCCTCCCTGCGCATCGGGGACTGGCTCAAGAAC	540	
Qy	577	GTCTGTGTCAACCCTGTATGAGAGGATGAGGACAAACACCTTCTGACTGAGAGGACAGAG	636	
Db	541	GTCTGTGTCAACCCTGTATGAGAGGATGAGGACAAACACCTTCTGACTGAGAGGACAGAG	600	
Qy	637	CTCGGGTGGAAGAGATCCCATGAGAATGAGAAGCCCTGGAGGCGAGGACACACCCCGTG	696	
Db	601	CTCGGGTGGAAGAGATCCCATGAGAATGAGAAGCCCTGGAGGCGAGGACACACCCCGTG	660	
Qy	697	GAGCTGTGCGCCGGACTTCGAGAGAACTATTAACATGTTACATCTTCCCTGTACACTGG	756	
Db	661	GAGCTGTGCGCCGGACTTCGAGAGAACTATTAACATGTTACATCTTCCCTGTACACTGG	720	


```

1  APPLICANT: Tanaka, Hiroaki
2  TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
3  FILE REFERENCE: 91.US6.DIV
4  CURRENT APPLICATION NUMBER: US/10/000,489
5  CURRENT FILING DATE: 2001-11-14
6  PRIOR APPLICATION NUMBER: US 09/924,340
7  PRIOR FILING DATE: 2001-08-06
8  PRIOR APPLICATION NUMBER: PCT/IB01/01715
9  PRIOR FILING DATE: 2001-08-06
10 PRIOR APPLICATION NUMBER: US 60/305,456
11 PRIOR FILING DATE: 2001-07-13
12 PRIOR APPLICATION NUMBER: US 60/302,277
13 PRIOR FILING DATE: 2001-06-29
14 PRIOR APPLICATION NUMBER: US 60/298,698
15 PRIOR FILING DATE: 2001-06-15
16 PRIOR APPLICATION NUMBER: US 60/293,574
17 PRIOR FILING DATE: 2001-05-25
18 NUMBER OF SEQ ID NOS: 112
19 SOFTWARE: Jpatent
20 SEQ ID NO 19
21 LENGTH: 844
22 TYPE: DNA
23 ORGANISM: Homo sapiens
24 FEATURE:
25 NAME/KEY: 5'UTR
26 LOCATION: 1..111
27 NAME/KEY: CDS
28 LOCATION: 112..813
29 NAME/KEY: 3'UTR
30 LOCATION: 814..844
31 US-10-000-489-19

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Query Match	33.5%	Score 713.6	DB 4	Length 844
Best Local Similarity	99.4%	Prod. No. 1.4e-179		
Matches 716	Conservative	0	Mismatches 4	Indels 0
Gaps	0			
Qy	1	CGGAGAGCGGCTCTGCTCGCGCTCGCTCGCTCGCTCGCCACGTAGAGGTTCCACGACCAATG	60	
Db	55	CCGGAGAGCGGCTCTGCTCGCGCTCGCTCGCTCGCTCGCCACGTAGAGGTTCCACGACCAATG	114	
Qy	61	AGGCGCTGGATCTTTCTTTCTCTTTGCTGCGCGGAGGGGCTTTGGCAGCGCCCTCAGCAA	120	
Db	115	AGGCGCTGGATCTTTCTTTCTCTTTGCTGCGCGGAGGGGCTTTGGCAGCGCCCTCAGCAA	174	
Qy	121	GAAGCCCTGCTGATGACAGAGGTGGTGCAGAAACTGTGGCAGAGGTGACTGAGGTA	180	
Db	175	GAAGCCCTGCTGATGACAGAGGTGGTGCAGAAACTGTGGCAGAGGTGACTGAGGTA	234	
Qy	181	TCTGTGGGAGCTAATCTCTGTCCAGGTGGAAGTATGAGAGAAATTTGATGATGTGGCAGAGAA	240	
Db	235	TCTGTGGGAGCTAATCTCTGTCCAGGTGGAAGTATGAGAGAAATTTGATGATGTGGCAGAGAA	294	
Qy	241	ACCGAAGAGGAGTGGTGGCGGAAAAATCCCTGCCAGAAACCACTGCAAAACAGCGCAAG	300	
Db	295	ACCGAAGAGGAGTGGTGGCGGAAAAATCCCTGCCAGAAACCACTGCAAAACAGCGCAAG	354	
Qy	301	GTGTGCCAGCTGGATGAGAAACACACCCCATGTGCGTGTGCCAGGACCCACCAAGCTGC	360	
Db	355	GTGTGCCAGCTGGATGAGAAACACACCCCATGTGCGTGTGCCAGGACCCACCAAGCTGC	414	
Qy	361	CCAGCCCCCATTTGGCGAGTTTGGAGAGGTGTGCAGCAATGACAAACAAGACCTTCGACTCT	420	
Db	415	CCAGCCCCCATTTGGCGAGTTTGGAGAGGTGTGCAGCAATGACAAACAAGACCTTCGACTCT	474	
Qy	421	TCCTGCCACATTTTGGCCAAAGTGCACCTCTGGAGGGCAACAAAGAGGGGCCAACAGCTC	480	
Db	475	TCCTGCCACATTTTGGCCAAAGTGCACCTCTGGAGGGCAACAAAGAGGGGCCAACAGCTC	534	
Qy	481	CACCTGACTACATCGGGCTTGCATAATACATCCCCCTTCGCTGGAATCTGAGCTGACC	540	
Db	535	CACCTGACTACATCGGGCTTGCATAATACATCCCCCTTCGCTGGAATCTGAGCTGACC	594	
Qy	541	GAATTCCTCCCTCGCGCATGCGGGAATGGCTCAAGAACGTCTCTGGTCAACCTCTATGAGAGG	600	

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Db      595  GAATTCCTCCCTGCGCATGCGGGACTGGCTCAAGAACGCTCCTGGTCACCTCTGTATGAGAGG 654
Qy      601  GATGAGGACAAACAACCTTTCTGACTGAGAAGCAGAGACTGCGGGTGAAGAAGATCCATGAG 660
Db      655  GATGAGGACAAACAACCTTCTGACTGAGAAGCAGAGACTGCGGGTGAAGAAGATCCATGAG 714
Qy      661  AATGAGAAGCGCCTGGAGGCAAGGAGACCAACCCCTGGAGAGCTGCTGCCCCGGGACTTCGAG 720
Db      715  AATGAGAAGCGCCTGGAGGCAAGGAGACCAACCCCTGGAGAGCTGCTGCCCCGGGACTTCGAG 774

RESULT 6
US-09-640-173-190
; Sequence 190, Application US/09640173
; Patent No. 6613515
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Stolk, John A.
; TITLE OF INVENTION: OVARIAN TUMOR SEQUENCES AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 210121.484C2
; CURRENT APPLICATION NUMBER: US/09/640.173
; CURRENT FILING DATE: 2000-08-15
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 190
; LENGTH: 481
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-640-173-190

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Query Match	22.0%	Score 469;	DB 4;	Length 481;
Best Local Similarity	99.8%;	Pred. No. 1.4e-114;		
Matches 480;	Conservative 0;	Mismatches 1;	Indels 1;	Gaps 1;
Qy	143	AGGTGGTGGGAAGAACTGTGSCA-GAGGTGACTGAGGTATCTGTGGGAGCTAAATCTCTGTC	201	
Db	1	AGGTGGTGGGAAGAACTGTGGCAGAGGTGACTGAGGTATCTGTGGGAGCTAAATCTCTGTC	60	
Qy	202	CAGGTGGAAGTAGGAGAAATTGTGATGTTGTCAGAGGAAACCGAAGAGGAGGTGTTGGCG	261	
Db	61	CAGGTGGAAGTAGGAGAAATTGTGATGTTGTCAGAGGAAACCGAAGAGGAGGTGTTGGCG	120	
Qy	262	GAATAATCCCTGCCAGAACCACTGCNAACACGCGAAGGTGTGCGAGCTGGATGAGAAC	321	
Db	121	GAATAATCCCTGCCAGAACCACTGCNAACACGCGAAGGTGTGCGAGCTGGATGAGAAC	180	
Qy	322	AACACCCCCATGTGCGTGTGCCAGACCCCAACACAGCTGCCACGCCCCCAATTTGGCGAGTTT	381	
Db	181	AACACCCCCATGTGCGTGTGCCAGACCCCAACACAGCTGCCACGCCCCCAATTTGGCGAGTTT	240	
Qy	382	GAGAAGGTGTGCAGCAATGCAACAAGACCTTTGACTCTTCTGTGCACCTTCTTTGCCACA	441	
Db	241	GAGAAGGTGTGCAGCAATGCAACAAGACCTTTGACTCTTCTGTGCACCTTCTTTGCCACA	300	
Qy	442	AAGTGCAACCTTGAGGGGCAACAAGAGGGGCCACAAGCTCCACCTGGACTACATCGGGCCT	501	
Db	301	AAGTGCAACCTTGAGGGGCAACAAGAGGGGCCACAAGCTCCACCTGGACTACATCGGGCCT	360	
Qy	502	TGCNAATACATCCCCCTTGCCTGGACTCTGAGCTGACCGGAATTCGCCCTCGGCATGGG	561	
Db	361	TGCNAATACATCCCCCTTGCCTGGACTCTGAGCTGACCGGAATTCGCCCTCGGCATGGG	420	
Qy	562	GACTGGCTCAAGAACGTCCTGGTCACCTGTATGAGAGGGATGAGGACAACAACCTTCTG	621	
Db	421	GACTGGCTCAAGAACGTCCTGGTCACCTGTATGAGAGGGATGAGGACAACAACCTTCTG	480	
Qy	622	A 622		
Db	481	A 481		

RESULT 7

US-09-713-550-190
; Sequence 190, Application US/09713550
; Patent No. 6617109
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Stolk, John A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; THERAPY AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.484C4
; CURRENT APPLICATION NUMBER: US/09/713,550
; CURRENT FILING DATE: 2000-11-14
; NUMBER OF SEQ ID NOS: 205
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 190
; LENGTH: 481
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-713-550-190

Query Match 22.0%; Score 469; DB 4; Length 481;
Best Local Similarity 99.8%; Pred. No. 1.4e-114;
Matches 480; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
Qy 143 AGGTGGTGAAGAACTGTGGCA-GAGTGACTGAGGTATCTGTGGAGCTTAATCCTGTC 201
Db 1 AGGTGGTGAAGAACTGTGGCAGAGTGACTGAGGTATCTGTGGAGCTTAATCCTGTC 60
Qy 202 CAGGTGGAAGTAGGAGAAATTTGATGTTGCAGAGAAACCCGAAGAGGAGGTGGTGGCG 261
Db 61 CAGGTGGAAGTAGGAGAAATTTGATGTTGCAGAGAAACCCGAAGAGGAGGTGGTGGCG 120
Qy 262 GAAATCCCTGCCAGAACCCACTGCAAAACACGGCAAGGTGCGAGCTGGATGAGAAC 321
Db 121 GAAATCCCTGCCAGAACCCACTGCAAAACACGGCAAGGTGCGAGCTGGATGAGAAC 180
Qy 322 AACACCCCTGCCAGAACCCACTGCAAAACACGGCAAGGTGCGAGCTGGATGAGAAC 381
Db 181 AACACCCCTGCCAGAACCCACTGCAAAACACGGCAAGGTGCGAGCTGGATGAGAAC 180
Qy 382 GAGAGGTGTGCAGCAATGACAAAGACCTTCGACTCTTCTGCCACTCTTTGGCCACA 441
Db 241 GAGAGGTGTGCAGCAATGACAAAGACCTTCGACTCTTCTGCCACTCTTTGGCCACA 300
Qy 442 AAGTGCACTTGGAGGGGACCAAGAGGGCCACAAGCTCCACCTGGAGTACATCGGCGCT 501
Db 301 AAGTGCACTTGGAGGGGACCAAGAGGGCCACAAGCTCCACCTGGAGTACATCGGCGCT 360
Qy 502 TGCAATACATCCCCCTTGGCTGCACTCTGAGCTGACCGAATTCCTCCCTGCGCATCGG 561
Db 361 TGCAATACATCCCCCTTGGCTGCACTCTGAGCTGACCGAATTCCTCCCTGCGCATCGG 420
Qy 562 GACTGGCTCAAGAACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 621
Db 421 GACTGGCTCAAGAACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
Qy 622 A 622
Db 481 A 481

RESULT 8

US-09-825-294-190
; Sequence 190, Application US/09825294
; Patent No. 6710170
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Stolk, John A.
; APPLICANT: Algate, Paul A.
; APPLICANT: Fling, Steven P.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; THERAPY AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.484C5

; CURRENT APPLICATION NUMBER: US/09/825,294
; CURRENT FILING DATE: 2001-04-03
; NUMBER OF SEQ ID NOS: 215
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 190
; LENGTH: 481
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-825-294-190

Query Match 22.0%; Score 469; DB 4; Length 481;
Best Local Similarity 99.8%; Pred. No. 1.4e-114;
Matches 480; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
Qy 143 AGGTGGTGAAGAACTGTGGCA-GAGTGACTGAGGTATCTGTGGAGCTTAATCCTGTC 201
Db 1 AGGTGGTGAAGAACTGTGGCAGAGTGACTGAGGTATCTGTGGAGCTTAATCCTGTC 60
Qy 202 CAGGTGGAAGTAGGAGAAATTTGATGTTGCAGAGAAACCCGAAGAGGAGGTGGTGGCG 261
Db 61 CAGGTGGAAGTAGGAGAAATTTGATGTTGCAGAGAAACCCGAAGAGGAGGTGGTGGCG 120
Qy 262 GAAATCCCTGCCAGAACCCACTGCAAAACACGGCAAGGTGCGAGCTGGATGAGAAC 321
Db 121 GAAATCCCTGCCAGAACCCACTGCAAAACACGGCAAGGTGCGAGCTGGATGAGAAC 180
Qy 322 AACACCCCTGCCAGAACCCACTGCAAAACACGGCAAGGTGCGAGCTGGATGAGAAC 381
Db 181 AACACCCCTGCCAGAACCCACTGCAAAACACGGCAAGGTGCGAGCTGGATGAGAAC 240
Qy 382 GAGAGGTGTGCAGCAATGACAAAGACCTTCGACTCTTCTGCCACTCTTTGGCCACA 441
Db 241 GAGAGGTGTGCAGCAATGACAAAGACCTTCGACTCTTCTGCCACTCTTTGGCCACA 300
Qy 442 AAGTGCACTTGGAGGGGACCAAGAGGGCCACAAGCTCCACCTGGAGTACATCGGCGCT 501
Db 301 AAGTGCACTTGGAGGGGACCAAGAGGGCCACAAGCTCCACCTGGAGTACATCGGCGCT 360
Qy 502 TGCAATACATCCCCCTTGGCTGCACTCTGAGCTGACCGAATTCCTCCCTGCGCATCGG 561
Db 361 TGCAATACATCCCCCTTGGCTGCACTCTGAGCTGACCGAATTCCTCCCTGCGCATCGG 420
Qy 562 GACTGGCTCAAGAACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 621
Db 421 GACTGGCTCAAGAACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
Qy 622 A 622
Db 481 A 481

RESULT 9

US-09-970-966-190
; Sequence 190, Application US/09970966
; Patent No. 6720146
; GENERAL INFORMATION:
; APPLICANT: Stolk, John A.
; APPLICANT: Moles, David Alan
; APPLICANT: Fling, Steven P.
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.484C6
; CURRENT APPLICATION NUMBER: US/09/970,966
; CURRENT FILING DATE: 2001-10-02
; NUMBER OF SEQ ID NOS: 215
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 190
; LENGTH: 481
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-970-966-190

Qy	1772	TTTTCAGCCGAGAGGCCAAAATCAAGAGTGGAGATGTGTAAGTGTGTAATAATAGAAAAAGT	1831
Db	121	TTTTCAGCCGAGAGGCCAAAATCAAGAGTGGAGATGTGTAAGTGTGTAATAATAGAAAAAGT	180
Qy	1832	GGAGTTGGTGAATCGGTTGTCTTTCTCCTCACATTTGGATGATGTGCATTAAGGTTTTTTAGC	1891
Db	181	GGAGTTGGTGAATCGGTTGTCTTTCTCCTCACATTTGGATGATGTGCATTAAGGTTTTTTAGC	240
Qy	1892	ATGTTCTCTCTTTTCTTTCACCCCTCCCTTTGTTCTCTATTAATCAAGAGAACTTCAAA	1951
Db	241	ATGTTCTCTCTTTTCTTTCACCCCTCCCTTTTCTTCTATTAATCAAGAGAACTTCAAA	300
Qy	1952	GTTAAATGGGATGTCGGATCTCACAGGCTGAGAACTCGTTTCACCTCCAAAGCATTTTCATGA	2011
Db	301	GTTAAATGGGATGTCGGATCTCACAGGCTGAGAACTCGTTTCACCTCCAAAGCATTTTCATGA	360
Qy	2012	AAAAGCTGCTCTTATTATTAATCATACAAACTCTCACCATGATGTGAAGAGTTTCACAAATC	2071
Db	361	AAAAGCTGCTCTTATTATTAATCATACAAACTCTCACCATGATGTGAAGAGTTTCACAAATC	420
Qy	2072	TTTCAAAATAAAAAGTAATGACTAGAAACTGAAAAAAA	2111
Db	421	TTTCAAAATAAAAAGTAATGACTAGAAACTGAAAAAAA	460

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RESULT 11
US-09-713-550-189
; Sequence 189, Application US/09713550
; Patent No. 6617109
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Stolk, John A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF OVARIAN
; FILE REFERENCE: 210121.484C4
; CURRENT APPLICATION NUMBER: US/09/713,550
; CURRENT FILING DATE: 2000-11-14
; NUMBER OF SEQ ID NOS: 205
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 189
; LENGTH: 460
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-713-550-189

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Query Match	21.1%;	Score 450.4;	DB 4;	Length 450;
Best Local Similarity	98.7%;	Pred. No. 1.2e-109;		
Matches 454;	Conservative 0;	Mismatches 6;	Indels 0;	Gaps 0;
Qy	1652	TTTTGGGACACGGACTGTCAAGTCTCTGGGAAGTGGTCAGCGCATCCTCGACGGGCTTCT	1711	
Db	1	TTTTGGGACACGGACTGTCAAGTCTCTGGGAAGTGGTCAGCGCATCCTCGACGGGCTTCT	60	
Qy	1712	CCTCCTCTGTCTTTTGGGAACACGAGGCTCTTCTCAGGGGCTCTAGGGATCGCAGGCTG	1771	
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Qy	1772	TTTTCAGCGAGGAAGGCCAAAATCAAGAGTGAGATGTAGAAAGTTGTAAATAAGAAAAGT	1831	
Db	121	TTTTCAGCGAGGAAGGCCAAAATCAAGAGTGAGATGTAGAAAGTTGTAAATAAGAAAAGT	180	
Qy	1832	GGAGTTGGTGCAATCGGTTGTCTTTTCCTCACATTTGGATGATGTCTAAGGTTTTTATGC	1891	
Db	181	GGAGTTGGTGCAATCGGTTGTCTTTTCCTCACATTTGGATGATGTCTAAGGTTTTTATGC	240	
Qy	1892	ATGTTCTCTCTTTCTTCTCACCTCCCTCTTTGTTCTTCTATTAAATCAAGAGAAACTTCAAA	1951	
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Db	301	GTTAAATGGGATGTCGGATCTCAAGGCTGAGAACTCGTTTCACTCAAGCATTTTCATGA	360	

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Qy 2072 TTTCAAATAAAAAAGTAAATGACTTAGAAACTGAAAAAAA 2111
Db 421 CTTCAAATAAAAAAGTAAATGACTTAGAAACTGAAAAAAA 460

RESULT 12

US-09-825-294-189
; Sequence 189, Application US/09825294
; Patent No. 6710170
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Stolk, John A.
; APPLICANT: Algate, Paul A.
; APPLICANT: Fling, Steven P.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TITL OF INVENTION: THERAPY AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.484C5
; CURRENT APPLICATION NUMBER: US/09/825,294
; CURRENT FILING DATE: 2001-04-03
; NUMBER OF SEQ ID NOS: 215
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 189
; LENGTH: 460
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-825-294-189

Query Match 21.1%; Score 450.4; DB 4; Length 460;
Best Local Similarity 98.7%; Pred. No. 1.2e-109;
Matches 454; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Qy 1652 TTTTGGGAGCAGCGACTGTCTGGAAGTGTCTGCGCATCTGCGAGGCTTCT 1711
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Qy 1712 CCTCCTCTGCTTTTGGGAACCGAGGCTCTTCTCAGGGCTCTAGGACTGCCAGGCTG 1771
Db 61 CCTCCTCTGCTTTTGGGAACCGAGGCTCTTCTCAGGGCTCTAGGACTGCCAGGCTG 120
Qy 1772 TTTCAAGCAGGAGCCAAATCAAGAGTGAGATGTAGAAAGTTGTAATAAGT 1831
Db 121 TTTCAAGCAGGAGCCAAATCAAGAGTGAGATGTAGAAAGTTGTAATAAGT 180
Qy 1832 GGAGTTGGTGAATCGGTGTTCTTCTCCTCAATTTGGATGATTGTCATAAGGTTTTTAGC 1891
Db 181 GGAGTTGGTGAATCGGTGTTCTTCTCCTCAATTTGGATGATTGTCATAAGGTTTTTAGC 240
Qy 1892 ATGTTCTCTCTTTTCTTCAACCTCCCTTTGTTCTTCTTATTAATCAAGAGAACTTCAAA 1951
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Qy 1952 GTTAATGGATGGTGGATCTCAGGCTGAGACTGTTCACTCCAAGCATTTTCATGA 2011
Db 301 GTTAATGGATGGTGGATCTCAGGCTGAGACTGTTCACTCCAAGCATTTTCATGA 360
Qy 2012 AAAAGCTGCTTCTTATTAAATCATACAAACTCTCACCATGATGTGAAGAGTTTCACAAATC 2071
Db 361 AAAAGCTGCTTCTTATTAAATCATACAAACTCTCACCATGATGTGAAGAGTTTCACAAATC 420
Qy 2072 TTTCAAATAAAAAAGTAAATGACTTAGAAACTGAAAAAAA 2111
Db 421 CTTCAAATAAAAAAGTAAATGACTTAGAAACTGAAAAAAA 460

RESULT 13

US-09-970-966-189
; Sequence 189, Application US/09970966
; Patent No. 6720146
; GENERAL INFORMATION:

; APPLICANT: Stolk, John A.
; APPLICANT: Molesch, David Alan
; APPLICANT: Fling, Steven P.
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITL OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.484C6
; CURRENT APPLICATION NUMBER: US/09/970,966
; CURRENT FILING DATE: 2001-10-02
; NUMBER OF SEQ ID NOS: 215
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 189
; LENGTH: 460
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-970-966-189

Query Match 21.1%; Score 450.4; DB 4; Length 460;
Best Local Similarity 98.7%; Pred. No. 1.2e-109;
Matches 454; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Qy 1652 TTTTGGGAGCAGCGACTGTCTGGAAGTGTCTGCGCATCTGCGAGGCTTCT 1711
Db 1 TTTTGGGAGCAGCGACTGTCTGGAAGTGTCTGCGCATCTGCGAGGCTTCT 60
Qy 1712 CCTCCTCTGCTTTTGGGAACCGAGGCTCTTCTCAGGGCTCTAGGACTGCCAGGCTG 1771
Db 61 CCTCCTCTGCTTTTGGGAACCGAGGCTCTTCTCAGGGCTCTAGGACTGCCAGGCTG 120
Qy 1772 TTTCAAGCAGGAGCCAAATCAAGAGTGAGATGTAGAAAGTTGTAATAAGT 1831
Db 121 TTTCAAGCAGGAGCCAAATCAAGAGTGAGATGTAGAAAGTTGTAATAAGT 180
Qy 1832 GGAGTTGGTGAATCGGTGTTCTTCTCCTCAATTTGGATGATTGTCATAAGGTTTTTAGC 1891
Db 181 GGAGTTGGTGAATCGGTGTTCTTCTCCTCAATTTGGATGATTGTCATAAGGTTTTTAGC 240
Qy 1892 ATGTTCTCTCTTTTCTTCAACCTCCCTTTGTTCTTCTTATTAATCAAGAGAACTTCAAA 1951
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Qy 1952 GTTAATGGATGGTGGATCTCAGGCTGAGACTGTTCACTCCAAGCATTTTCATGA 2011
Db 301 GTTAATGGATGGTGGATCTCAGGCTGAGACTGTTCACTCCAAGCATTTTCATGA 360
Qy 2012 AAAAGCTGCTTCTTATTAAATCATACAAACTCTCACCATGATGTGAAGAGTTTCACAAATC 2071
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RESULT 14

US-09-513-999C-141
; Sequence 141, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961

; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 141
; LENGTH: 490

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Title: US-09-340-595A-1
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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 3: Geneseqn2000s:*
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- 12: Geneseqn2004as:*
- 13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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7	2133	100.0	2133	8	ADQ8129 Human SPA
8	2133	100.0	2133	10	ADQ85221 Farnesyl
9	2133	100.0	2133	10	ADQ81423 Leukaemia
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ALIGNMENTS

RESULT 1

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ID AAH76473 standard; cDNA; 2133 BP.

AC AAH76473;

DT 22-OCT-2001 (first entry)

DE cDNA corresponding to human IFN-alpha induced gene encoding SPARC.
KW Human; interferon-alpha induced gene; type I interferon treatment;
KW chronic viral hepatitis; relapsing remitting multiple sclerosis;
KW neoplastic disease; SPARC; IFN-alpha; interferon-alpha; ss.

OS Homo sapiens.

FH Key Location/Qualifiers
FT CDS 58..969

FT FT /*tag= a

FT FT /product= "SPARC"

PN WO200159155-A2.

XX 16-AUG-2001.

XX 09-FEB-2001; 2001WO-GB000578.

XX 11-FEB-2000; 2000GB-00003203.

XX 11-FEB-2000; 2000GB-00003204.

XX 11-FEB-2000; 2000GB-00003205.

XX 11-FEB-2000; 2000GB-00003206.

XX 11-FEB-2000; 2000GB-00003207.

XX 11-FEB-2000; 2000GB-00003208.

XX 11-FEB-2000; 2000GB-00003210.

XX 11-FEB-2000; 2000GB-00003212.

XX 11-FEB-2000; 2000GB-00003213.

XX 11-FEB-2000; 2000GB-00003215.

XX 11-FEB-2000; 2000GB-00003216.

XX 11-FEB-2000; 2000GB-00003219.

XX 11-FEB-2000; 2000GB-00003220.

XX 11-FEB-2000; 2000GB-00003221.

XX 11-FEB-2000; 2000GB-00003222.

XX 17-FEB-2000; 2000GB-00003768.

OS	Homo sapiens.	
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XX	WO200194629-A2.	
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XX		
XX	13-DEC-2001.	
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XX	30-MAY-2001; 2001WO-US010838.	
XX		
PR	05-JUN-2000; 2000US-0209473P.	
PR	05-JUN-2000; 2000US-0209531P.	
PR	18-SEP-2000; 2000US-0233133P.	
PR	18-SEP-2000; 2000US-0233617P.	
PR	20-SEP-2000; 2000US-0234009P.	
PR	20-SEP-2000; 2000US-0234034P.	
PR	20-SEP-2000; 2000US-0234052P.	
PR	22-SEP-2000; 2000US-0234509P.	
PR	22-SEP-2000; 2000US-0234567P.	
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PR	25-SEP-2000; 2000US-0235077P.	
PR	25-SEP-2000; 2000US-0235082P.	
PR	25-SEP-2000; 2000US-0235134P.	
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RESULT 5

ABN95593

ID ABN95593 standard; DNA; 2133 BP.

XX AC ABN95593;

XX DT 13-AUG-2002 (first entry)

XX DE Gene #2091 used to diagnose liver cancer.

XX KW Gene; liver cancer; ds; hepatocellular carcinoma; hepatotropic;
metastatic liver tumour; cytostatic; expression profile; disease state;
disease progression; drug toxicity; drug efficacy; drug metabolism.

XX OS Homo sapiens.

XX PN WO200229103-A2.

XX PD 11-APR-2002.

XX PF 02-OCT-2001; 2001WO-US030589.

XX PR 02-OCT-2000; 2000US-0237054P.

XX (GENE-) GENE LOGIC INC.

XX PI Horne D, Alvares C, Peres-Da-Silva S, Vockley JG;

XX DR WPI; 2002-426119/45.

XX PT Diagnosing and detecting the progression of liver cancer, hepatocellular
carcinoma or metastatic liver tumor in a patient, involves detecting the
level of expression of two or more genes in a liver tissue sample.

XX PS Claim 1; SEQ ID NO 2091; 298pp; English.

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1261 CTGGGCTCTGCTTTAAACACACATTCGAGCTTCAACTTTTCTCTTTAGTGTCTCTGTTGA 1320
Dd |||||
1261 CTGGGCTCTGCTTTAAACACACATTCGAGCTTCAACTTTTCTCTTTAGTGTCTCTGTTGA 1320
Qy |||||
1321 AACTAATACTTACCAGGTGACACTTTGTGTCTATTTCAATTTCAAGGGTCTTGGCTGCTGT 1380
Dd |||||
1321 AACTAATACTTACCAGGTGACACTTTGTGTCTATTTCAATTTCAAGGGTCTTGGCTGCTGT 1380
Qy |||||
1381 GGGCTTCCCGAGGTGGCTGGAGGTGGGCAAGGAGTAACAGACACACAGCATCTGTCA 1440
Dd |||||
1381 GGGCTTCCCGAGGTGGCTGGAGGTGGGCAAGGAGTAACAGACACACAGCATCTGTCA 1440
Qy |||||
1441 AGGATGGTTTTGGGACTAGAGGCTCAGTGTGGGAGAGATCCCTGCGAGAATCCACCAACC 1500
Dd |||||
1441 AGGATGGTTTTGGGACTAGAGGCTCAGTGTGGGAGAGATCCCTGCGAGAATCCACCAACC 1500
Qy |||||
1501 AGAAGTGGTTTTGGCTGAGGCTGTAACTGAGAGAAAGATTCCTGGGCTGTCTTATGAATA 1560
Dd |||||
1501 AGAAGTGGTTTTGGCTGAGGCTGTAACTGAGAGAAAGATTCCTGGGCTGTCTTATGAATA 1560
Qy |||||
1561 TATAGACATTTCTACATAGGCCAGTTCATCAGCATTTCTCTCTTTACCTTTTCAGTGTGAG 1620
Dd |||||
1561 TATAGACATTTCTACATAGGCCAGTTCATCAGCATTTCTCTCTTTACCTTTTCAGTGTGAG 1620
Qy |||||
1621 TTTCTTTTCACTTAGGCTGTGTTTCAAACTTTTGGGAGCAGGACTGTCTGTTCTCTG 1680
Dd |||||
1621 TTTCTTTTCACTTAGGCTGTGTTTCAAACTTTTGGGAGCAGGACTGTCTGTTCTCTG 1680
Qy |||||
1681 GGAAGTGGTCAGCGCATCTCTGAGGCTTCTCTCTCTCTCTTCTTGGAGAACAGGGCT 1740
Dd |||||
1681 GGAAGTGGTCAGCGCATCTCTGAGGCTTCTCTCTCTCTCTTCTTGGAGAACAGGGCT 1740
Qy |||||
1741 CTCTCTCAGGGGCTCTAGGAGCTGCGAGGCTGTTTCAAGCAGGAGGCGCAAAATCAAGAGT 1800
Dd |||||
1741 CTCTCTCAGGGGCTCTAGGAGCTGCGAGGCTGTTTCAAGCAGGAGGCGCAAAATCAAGAGT 1800
Qy |||||
1801 GAGATGTAGAAAGTTGTAAATAGAAAAGTGGAGTGGTGAATCGGTGTCTTCTCTC 1860
Dd |||||
1801 GAGATGTAGAAAGTTGTAAATAGAAAAGTGGAGTGGTGAATCGGTGTCTTCTCTC 1860
Qy |||||
1861 ACATTTGGATGATTTGATAGAGTTTGTAGCATGTTCTCTCTCTCTCTCTCTCTCTCTCTCT 1920
Dd |||||
1861 ACATTTGGATGATTTGATAGAGTTTGTAGCATGTTCTCTCTCTCTCTCTCTCTCTCTCTCT 1920
Qy |||||
1921 TGTCTCTCTAATTAATCAAGAGAACTTCAAAAGTTAATGGAGTGTGCGATCTCACAGGCT 1980
Dd |||||
1921 TGTCTCTCTAATTAATCAAGAGAACTTCAAAAGTTAATGGAGTGTGCGATCTCACAGGCT 1980
Qy |||||
1981 GAGAACTCGTTTCACTTCAAGCATTTCTATGAAAAAGTGTCTTCTTATTAATCATCAAAAC 2040
Dd |||||
1981 GAGAACTCGTTTCACTTCAAGCATTTCTATGAAAAAGTGTCTTCTTATTAATCATCAAAAC 2040

Qy 2041 TCTCACCATGATGTGAGAGCTTTTCACAAATCTTTCAAAATATAAAAGTAATGACTTAGAAA 2100
Dd |||||
2041 TCTCACCATGATGTGAGAGCTTTTCACAAATCTTTCAAAATATAAAAGTAATGACTTAGAAA 2100
Qy 2101 CTGAAAAAATTT 2133
Dd |||||
2101 CTGAAAAAATTT 2133
Qy 2101 CTGAAAAAATTT 2133
Dd |||||
RESULT 7
AAD48129
ID AAD48129 standard; DNA; 2133 BP.
XX AAD48129;
XX DT 24-FEB-2003 (first entry)
XX Human SPARC (osteonectin) DNA.
XX Brain; tumour protein target; Tbt; ischaemic stroke; cancer; epilepsy;
KW schizophrenia; depression; Alzheimer's disease; Parkinson's disease;
KW Huntington's chorea; traumatic head injury; dementia; stupor; headache;
KW coma; vertigo; weakness; myasthenia gravis; cerebrovascular disorder;
KW infection; multiple sclerosis; pregnancy; medical illness; vasotropic;
KW metabolic deficiency; cerebroprotective; antidepressant; antibacterial;
KW cytosolic; neotropic; analgesic; fungicide; virucide; human; SPARC;
KW osteonectin; gene; ds.
XX Homo sapiens.
OS
XX Key Location/Qualifiers
XX CDS 58..969
XX /*tag= a
XX /product= "Human SPARC (osteonectin) protein"
XX WO200276510-A1.
XX 03-OCT-2002.
XX 22-MAR-2002; 2002WO-US008992.
XX 23-MAR-2001; 2001US-00816703.
XX 17-OCT-2001; 2001US-00983000.
XX (AGYT-) AGY THERAPEUTICS INC.
XX Mueller S, Melcher T, Chin DJ;
XX WPI: 2003-029903/02.
XX P-PSDB; AAE30335.
XX Developing active agents that modulate the activity of a brain tumor
XX protein target gene or gene product for treating e.g. stroke or cancer,
XX comprises contacting an agent with a brain tumor protein.
XX Claim 1; Page 100-103; 135pp; English.
XX The invention relates to a method for developing biologically active
XX agents that modulate activity of a brain tumour protein target (Tbt) gene
XX or gene product. The method is useful for developing biologically active
XX agents that modulate the activity of a brain tumour protein target gene
XX or gene product. Compounds that bind to the brain tumour proteins are
XX useful for treating e.g. ischaemic stroke, brain cancer, epilepsy,
XX schizophrenia, depression, Alzheimer's disease, Parkinson's disease,
XX Huntington's chorea, traumatic head injury, dementia, stupor, headache,
XX coma, vertigo, weakness, myasthenia gravis, cerebrovascular disorders,
XX infectious disorders (including fungal, bacterial, viral and parasitic
XX infections), multiple sclerosis, and other complications associated with
XX pregnancy, medical illness, alcohol and substance abuse, toxins and
XX metabolic deficiencies. The brain tumour proteins may also be used to
XX raise antibodies. The present sequence is human SPARC (osteonectin) DNA
XX used to illustrate the method of the invention


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Db 481 |CACCTGACCTACATCGGGCTTGCATAATACATCCCCCTTGGCTGGACTCTGAGTGACC 540|
Qy 541 |GAATTTCCCTCGCGCATCGCGGACTGGCTCAAGAACGTCCTGGTCACTCCCTGTATGAGAG 600|
Db 541 |GAATTTCCCTCGCGCATCGCGGACTGGCTCAAGAACGTCCTGGTCACTCCCTGTATGAGAG 600|
Qy 601 |GATGAGACAAACACTTCTGACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660|
Db 601 |GATGAGACAAACACTTCTGACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660|
Qy 661 |AATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720|
Db 661 |AATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720|
Qy 721 |AAGAACTATAACATGTATACATCTTCCCTGTACATCTGGCAGTTCCGCCAGCTGGACAGCAC 780|
Db 721 |AAGAACTATAACATGTATACATCTTCCCTGTACATCTGGCAGTTCCGCCAGCTGGACAGCAC 780|
Qy 781 |CCCATGAGCGGATACCTCTCCCAACCGAGTGCTCCACTGGTGCTCCCTCATCCCC 840|
Db 781 |CCCATGAGCGGATACCTCTCCCAACCGAGTGCTCCACTGGTGCTCCCTCATCCCC 840|
Qy 841 |ATGAGCATTTGCACACCCCGCTTTTCGAGACCTGTGACCTGGACATGACAGTACATC 900|
Db 841 |ATGAGCATTTGCACACCCCGCTTTTCGAGACCTGTGACCTGGACATGACAGTACATC 900|
Qy 901 |GCCCTGATGAGTGGGCGGCTGCTCCGCATCAAGCAGAGAGATATCGACAAGGATCTT 960|
Db 901 |GCCCTGATGAGTGGGCGGCTGCTCCGCATCAAGCAGAGAGATATCGACAAGGATCTT 960|
Qy 961 |GTGATCTAAATCCACTCTTCCACAGTACCGGATCTCTTTAACTCCCTCCCTCGTGT 1020|
Db 961 |GTGATCTAAATCCACTCTTCCACAGTACCGGATCTCTTTAACTCCCTCCCTCGTGT 1020|
Qy 1021 |TTCCCCCAATGTTTAAATGTTTGGATGTTGTTGTTCTGCTGGAGACAGAGTGCTAA 1080|
Db 1021 |TTCCCCCAATGTTTAAATGTTTGGATGTTGTTGTTCTGCTGGAGACAGAGTGCTAA 1080|
Qy 1081 |CATAGATTTAAGTGAATACATTAACCGTGTCTAAATAATGAATAATCTAACCCCAAGACATGA 1140|
Db 1081 |CATAGATTTAAGTGAATACATTAACCGTGTCTAAATAATGAATAATCTAACCCCAAGACATGA 1140|
Qy 1141 |CATCTTTAGCTGTAACCTTAATTAAGGCTTTTCCACAGCATTAATAGTCCCATTTT 1200|
Db 1141 |CATCTTTAGCTGTAACCTTAATTAAGGCTTTTCCACAGCATTAATAGTCCCATTTT 1200|
Qy 1201 |TCTCTGCCATTTCTAGCTTTGCCATTTCTTATGGCACATGGGTGGACACGGATCTG 1260|
Db 1201 |TCTCTGCCATTTCTAGCTTTGCCATTTCTTATGGCACATGGGTGGACACGGATCTG 1260|
Qy 1261 |CTGGGCTCTGCTTTAAACACACATTCGAGCTTCAACTTTTCTTTAGTGTCTTGTTGA 1320|
Db 1261 |CTGGGCTCTGCTTTAAACACACATTCGAGCTTCAACTTTTCTTTAGTGTCTTGTTGA 1320|
Qy 1321 |AACTAATACTTACCGAGTCAGACTTGTGTGTTCAATTTCAATTTAGTGTCTTGTTGA 1380|
Db 1321 |AACTAATACTTACCGAGTCAGACTTGTGTGTTCAATTTCAATTTAGTGTCTTGTTGA 1380|
Qy 1381 |GGGCTTCCCGAGTGGCTGGAGTGGGCAAGGAAGTAAACACACACAGATCTGTCA 1440|
Db 1381 |GGGCTTCCCGAGTGGCTGGAGTGGGCAAGGAAGTAAACACACACAGATCTGTCA 1440|
Qy 1441 |AGGATGTTTTGGGACTAGAGGCTCAGTGGTGGGAGAGATCCCTGCAGAAATCCCAACACC 1500|
Db 1441 |AGGATGTTTTGGGACTAGAGGCTCAGTGGTGGGAGAGATCCCTGCAGAAATCCCAACACC 1500|
Qy 1501 |AGACGTTGTTGGCTGAGGCTGTAATGAGAGAAAGTCTGGGGCTGCTTATGAAA 1560|
Db 1501 |AGACGTTGTTGGCTGAGGCTGTAATGAGAGAAAGTCTGGGGCTGCTTATGAAA 1560|
Qy 1561 |TATAGACATTTCTACATAAGCCAGTTTCATCACCATTCTCTCTTACCTTTAGTGCAG 1620|
Db 1561 |TATAGACATTTCTACATAAGCCAGTTTCATCACCATTCTCTCTTACCTTTAGTGCAG 1620|
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Db 1561 |TATAGACATTTCTACATAAGCCAGTTTCATCACCATTCTCTCTTACCTTTAGTGCAG 1620|
Qy 1621 |TTTCTTTTTCATATAGGCTGTGGTTCAAACTTTTGGAGACAGGACTGTCACTTCTGTG 1680|
Db 1621 |TTTCTTTTTCATATAGGCTGTGGTTCAAACTTTTGGAGACAGGACTGTCACTTCTGTG 1680|
Qy 1681 |GGAAGTGGTCAGCGCATCTCGCAGGGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1740|
Db 1681 |GGAAGTGGTCAGCGCATCTCGCAGGGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1740|
Qy 1741 |CTTCTCAGGGGCTCTAGGGACTCGCAGGGCTGTTCAGCCAGGAGGCCAAAATCAAGAGT 1800|
Db 1741 |CTTCTCAGGGGCTCTAGGGACTCGCAGGGCTGTTCAGCCAGGAGGCCAAAATCAAGAGT 1800|
Qy 1801 |GAGATGTAGAAAGTGTGTAAATAGAAAAAGTGAGTTGGTGAATCGGTTGTTCTTCTC 1860|
Db 1801 |GAGATGTAGAAAGTGTGTAAATAGAAAAAGTGAGTTGGTGAATCGGTTGTTCTTCTC 1860|
Qy 1861 |ACATTTGGATGATGTGCATAAGGTTTTCAGCATGTTCTCTCTCTCTCTCTCTCTCTCT 1920|
Db 1861 |ACATTTGGATGATGTGCATAAGGTTTTCAGCATGTTCTCTCTCTCTCTCTCTCTCTCT 1920|
Qy 1921 |TGTCTCTTCTAATTAATCAAGAGAACTTCAAAAGTTAATGGATGGTTCGGATCTCACAGGCT 1980|
Db 1921 |TGTCTCTTCTAATTAATCAAGAGAACTTCAAAAGTTAATGGATGGTTCGGATCTCACAGGCT 1980|
Qy 1981 |GAGAACTCGTTCACCTCCAGAGCATTTTCATGAAAAGCTGCTTCTTATTAATCATACAAAC 2040|
Db 1981 |GAGAACTCGTTCACCTCCAGAGCATTTTCATGAAAAGCTGCTTCTTATTAATCATACAAAC 2040|
Qy 2041 |TCTCACCATGATCTGGAAGGTTTCACAAATCTTTCAAAATAAAAAAGTAATGACTTAGAAA 2100|
Db 2041 |TCTCACCATGATCTGGAAGGTTTCACAAATCTTTCAAAATAAAAAAGTAATGACTTAGAAA 2100|
Qy 2101 |CTGAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA 2133|
Db 2101 |CTGAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA 2133|
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RESULT 10

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ADH28881
ID ADH28881 standard; DNA; 2133 BP.
XX
AC ADH28881;
XX
XX 11-MAR-2004 (first entry)
XX
DE Human chronic myelogenous leukaemia (CML) gene marker #149.
XX
KW ds; chronic phase chronic myelogenous leukaemia; CP-CML;
KW blast crisis CML; BC-CML; human; chronic myelogenous leukaemia;
KW gene marker.
XX
OS Homo sapiens.
XX
XX US2003104426-A1.
XX
XX 05-JUN-2003.
XX
XX 14-JUN-2002; 2002US-00171581.
XX
XX 18-JUN-2001; 2001US-0298914P.
XX
XX (LINSLEY P S.
XX (MAOM/) MAO M.
XX (DAIH/) DAI H.
XX (HEY/) HE Y.
XX (RADJ/) RADICH J P.
XX
XX Linsley PS, Mao M, Dai H, He Y, Radich JP;
XX WPI; 2003-787046/74.
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Classifying cell sample as chronic phase chronic myelogenous leukemia or blast crisis chronic myelogenous leukemia by detecting difference in expression of genes corresponding to the markers such as X15415, U89436.

The invention relates to a method of classifying a cell sample as chronic phase chronic myelogenous leukaemia (CP-CML) or blast crisis CML (BC-CML). The method is useful for classifying a sample as CP-CML or BC-CML. The present sequence represents a human chronic myelogenous leukaemia (CML) gene marker used to distinguish blast crisis CML from chronic phase CML.

Sequence 2133 BP; 543 A; 533 C; 521 G; 536 T; 0 U; 0 Other;

Query Match 100.0%; Score 2133; DB 10; Length 2133;

Best Local Similarity 100.0%; Pred. No. 0;
Matches 2133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 CGGAGAGCGGCTCTGCCCTGCCGCTGCCACTGAGGGTCCCAGCACCATG 60

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CGGAGAGCGCGCTCTGCCCTGCCCTGCCCTGCCCACTGAGGGTCCCAGCACCATG 60

61 AGGGCCTGGATCTTCTTTCTCCTTGGCCGGAGGGCCTTGGCAGCCCTCAGCAA 120

Year	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100
1990	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100											
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1992	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100											
1993	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66</																																													

61 AGGGCCCTGGATCTTCCTTCTCCTTTGCCCAGGCCCTTGGCAGCCCCCTCAGCAA 120

121 GAAGCCCTGCCTGATGAGACAGAGGTGGTGGAACTGTGGCAGAGGTGACTGAGGTA 180 y

b 121 GAAGCCCTGCCTGATGAGACAGAGGTGGTGGGAAGAACTGTGGCAGAGGTCACTGACGTA 180

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791 CCCCTTCGACCCGGTATCCCTCCTCCCACCCCGCCGCTGCCTCCCTCATCCCC
840

Y /BI CCCATTGACGGGTACCCTCCACACCGAGCTGGTTCACATGCTGCATCCCCC

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Db |||||
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RESULT 15

ADR25011

ID ADR25011 standard; DNA; 2133 BP.

XX ADR25011;

XX AC ADR25011;

XX DT 21-OCT-2004 (first entry)

XX DE Breast cancer prognosis marker #872.

XX ds; breast cancer; prognosis; gene expression; diagnosis.

XX OS Homo sapiens.

XX PN WO2004065545-A2.

XX XX 05-AUG-2004.

XX PF 15-JAN-2004; 2004WO-US001100.

XX XX 15-JAN-2003; 2003US-00342887.

XX PR (ROSE-) ROSETTA INPHARMATICS LLC.

XX PA (NECA-) NETHERLANDS CANCER INST.


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Search completed: May 9, 2005, 22:26:53
Job time : 1078 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 10, 2005, 00:56:13 ; Search time 4544 Seconds
(without alignments)
2870.240 Million cell updates/sec

Title: US-09-340-595A-1
Perfect score: 2133
Sequence: 1 cgggagcgcgctgtgctt.....aaaaaaaaaaaaaaaaaaaaa 2133

Scoring table: IDENTITY NUC
Gapop 10_0 , Gapext 1.0

Searched: 5654200 seqs, 3057283753 residues

Total number of hits satisfying chosen parameters: 11308400

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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OM nucleic - nucleic search, using sw model

Run on: May 9, 2005, 22:26:58 / Search time 2435 Seconds
(without alignments)
1801.979 Million cell updates/sec

Title: US-09-340-595A-1
Perfect score: 2133
Sequence: 1 cggagagcgctctgcct.....aaaaaaaaaaaaaaaaaaaa 2133

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 9398789 seqs, 102855566 residues

Total number of hits satisfying chosen parameters: 18797578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 9, 2005, 22:09:09 ; Search time 7285 Seconds
(without alignments)
11952.718 Million cell updates/sec

Title: US-09-340-595A-1
Perfect score: 2133
Sequence: 1 cggagagcgctctgcct.....aaaaaaaaaaaaaaaaa 2133

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 45554873 seqs, 20411521753 residues

Total number of hits satisfying chosen parameters: 91109746

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3	2133	100.0	2133	6	AX330482	AX330482 Sequence
4	2133	100.0	2133	6	AX409444	AX409444 Sequence
5	2133	100.0	2133	6	AX775122	AX775122 Sequence
6	2133	100.0	2133	6	AX779822	AX779822 Sequence
7	2133	100.0	2133	9	HUMSPARC	J03040 Human SPARC
8	2110.8	99.0	2114	9	BC004974	BC004974 Homo sapi
9	2095	98.2	3178	9	BC072457	BC072457 Homo sapi
10	2079.2	97.5	2089	9	BC008011	BC008011 Homo sapi
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16	1841	86.3	2035	6	AX096969	AX096969 Homo sapi
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18	1388.6	65.1	2141	4	BOVOSTAA	JQ3233 Bovine oste
19	1304	61.1	1516	6	BD204659	BD204659 Human nuc

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QY	301	GTGTGCCAGCTGGATGAGAACAAACACCCCAATGTGCGTGCCAGGACCCACCAAGCTGC	360
DB	301	GTGTGCCAGCTGGATGAGAACAAACACCCCAATGTGCGTGCCAGGACCCACCAAGCTGC	360
QY	361	CCAGCCCCATTTGGCGAGTTTGAAAGGTGTGCAGCAATGACAAACAAGACTTTCGACTCT	420
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QY	421	TCCTGCCACTTCTTTGGCACAAAGTGCACCTCGAGGGCCACCAAGAGGGCCACAGCTC	480
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DB	1201	TCTCTTGGCATTGTAGCTTTGGCCCATTTGCTTAATGGCACAATGGGTGGACAAGGATCTG	1260

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Qy	1321	AACATAACTTACCGAGTCAGACTTTCGTGTTCAATTCATTTACGGGTCTTTGGCTGCCTGT	1380
Db	1321	AACATAACTTACCGAGTCAGACTTTCGTGTTCAATTCATTTACGGGTCTTTGGCTGCCTGT	1380
Qy	1381	GGGCTTCCCAGGTGGCTCGAGTGGGCAAGAGTAACAGACACACGATGTTGTCTCA	1440
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Db	1441	AGGATGGTTTTGGAGCTAGAGGCTCAGTGTGGGAGAGATCCCTGCGAGATCCACCAACC	1500
Qy	1501	AGAACGTGGTTTTGGCTCGAGGCTGAACCTGAGAGAAAGATTCTGGGGCTGCTTATGAAAA	1560
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Qy	1561	TATAGACATTCTCACATAAGCCAGTTTCATCAACAATTTCTCTTTACCTTTTCAGTGCAG	1620
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Qy	1621	TTTTCTTTTTCATTTAGGCTCTGGTTCAAACCTTTTGGGAGCAGGACTGTCAGTTCCTCTG	1680
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Qy	1921	TGTTCTTCTATTAATCAAGAGAACTTCAAAGTTTAATGGAGTGGTCGGATCTCACAGGCT	1980
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Qy	1981	GAGAACTCGTTTCACCTCCAAGCATTTTCATGAAAAGTCGTCTCTTAATTAATCATACAAC	2040
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Qy	2101	CTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	2133
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DEFINITION	Sequence 31 from Patent WO0159155.		
ACCESSION	AX214552		
VERSION	AX214552.1	GI:15524595	
KEYWORDS	·		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
		linear	PAT 06-SEP-2001

[illegible]

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RESULT 4
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ACCESSION  AX409444
VERSION     AX409444.1  GI:21442149
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ORGANISM    Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Alvares,C., Horne,D., Peres-da-Silva,S. and Vockley,J.G.
TITLE       Gene expression profiles in liver cancer
JOURNAL     Patent: WO 0229103-A 2091 11-APR-2002;
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Qy	1321	AACCTAATACCTTACCGAGTCAGACTTTGTGTGTTCAATTCATTTCAGGGTCTTGGCTGCCTGT	1380
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Qy	1381	GGGCTTCCCAGGTGGCTCGAGTGGGGCAAGGAAAGTAGAACACACACAGATGTTCTCA	1440
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Qy	1621	TTTTCTTTTCACTAGGCTCTGGTTCAAACTTTTGGGAGCATGGACTGTCAGTTCTCTG	1680
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Qy	1681	GGAAGTGGTCAGGCGCATCTCGAGGGCTTCTCTCTCTCTCTTTTGGAGAACCAAGGCT	1740
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Qy	1741	CTTCTCAGGGGCTCAGGAGCTGCCAGGCTGTTTCAGCAGGAGGCCAAATCAAGAGT	1800
Db	1741	CTTCTCAGGGGCTCAGGAGCTGCCAGGCTGTTTCAGCAGGAGGCCAAATCAAGAGT	1800
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Qy	1861	ACATTGGATGATGTGCTAAGGTTTTAGCATGTTCTCTCTCTTCTTCAACCTCCCCCTT	1920
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Qy	1921	TGTTCTTCTAATTAATCAAGAGAACTTCAAAGTTAAATGGGATGGTCGGATCTCACAGGCT	1980
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Qy	1981	GAGAACTCGTTTACCTCCAAAGCATTTTCATCAAAAAGCTGCTCTTATTAATCATACAAC	2040
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Qy	2041	TCTCACCATCATGTGAGAGTTTTCAAAATCTTCAAAATAGAAAGTAATGACTTAGAAA	2100
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LOCUS	Human SPARC/osteonectin mRNA, complete cds.		
DEFINITION	J03040		
ACCESSION	J03040.1 GI:338312		
VERSION	calcium-binding protein; glycoprotein; osteonectin.		
KEYWORDS	Homo sapiens		
SOURCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
ORGANISM	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		

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Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield, Andy Chan, Steve S. Chand, William Chow, Alison Cloutier, Ruth Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao, Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Morin, Teika Olson, Diana Palmquist, Anca Petrescu, Anna Liisa Prabhuk, Parvaneh Saeedi, JR Santos, Angeliene Schnerch, Ursula Skaleka, Duane Smaitus, Jeff Scott, Miranda Tsai, George Yang, Jacquie Schein, Asim Siddiqui, Rob Holt, Marco Marra

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
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REFERENCE			
AUTHORS			
Isogai, T., Sugiyama, T., Otsuki, T., Wakamatsu, A., Sato, H., Ishii, S.,			
Yamanoto, J. I., Isono, Y., Hio, Y., Otsuka, K., Nagai, K., Irie, R.,			
Tamechika, I., Seki, N., Yoshikawa, T., Otsuka, M., Nagahari, K. and			
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Full-length cDNA sequences			
Patent: Ep 1308459-A 1310 07-MAY-2003;			
Helix Research Institute (JP) ; Research Association for			
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Qy	265	AATCCCTGCCAGAACCACTGCCAACCGCAAGGTGTGCCAGCTGGATGAGAACCAAC 324	
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VERSION	AK092877.1 GI:21751578		
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ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.		
AUTHORS	Ota, T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R., Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H., Sekine M., Oyayashi M., Nishi T., Shibahara T., Tanaka F., Ishii S., Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahori K., Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A., Sudo H., Hosoi T., Kaku Y., Kodaira H., Kondo H., Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K., Tanai H., Kimata M., Watanabe M., Hirao K., Chiba Y., Ishida S., Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Kusano J., Kanehori K., Takahashi-Fujii A., Hara H., Tanase T., Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N., Muesashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S., Yoshioka S., Matsunawa H., Ichihara T., Shiohata N., Sano S., Moriya S., Momiyama H., Satoh N., Takami S.,		

Terashima, Y., Suzuki, O., Nakagawa, S., Senoh, A., Mizoguchi, H., Goto, Y., Shimizu, P., Wakebe, H., Hishigaki, H., Watanabe, T., Sugiyama, A., Takenami, M., Kawakami, B., Yamazaki, M., Watanabe, K., Kumagai, A., Itakura, S., Fukuzumi, Y., Fujimori, Y., Komiyama, M., Tashiro, H., Tanigami, A., Fujiwara, T., Ono, T., Yamada, K., Fujii, Y., Ozaki, K., Hiroo, M., Ohmori, Y., Kawabata, A., Hiki, J., Kobatake, N., Inagaki, H., Ikema, Y., Okamoto, S., Okitani, R., Kawakami, T., Noguchi, S., Itoh, T., Shigeta, K., Senba, T., Matsumura, K., Nakajima, Y., Mizuno, T., Morinaga, M., Sasaki, M., Togashi, T., Oyama, M., Hata, H., Watanabe, M., Komatsu, T., Mizushima-Sugano, J., Satoh, T., Shirai, Y., Takahashi, Y., Nakagawa, K., Okumura, K., Nagase, T., Nomura, N., Kikuchi, H., Masuho, Y., Yamashita, R., Nakai, K., Yada, T., Nakamura, Y., Ohara, O., Isogai, T. and Sugano, S. Complete sequencing and characterization of 21,243 full-length human cDNAs
Nat. Genet. 36 (1), 40-45 (2004)

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Ishibaishi, T., Kanehori, K., Yosida, M., Watanabe, S., Ishida, S., Ono, Y., Hotuta, T., Hiraoka, S., Murakawa, K., Takiguchi, S., Kusano, J., Watanabe, M., Fujimori, K., Tanai, H., Ishida, M., Yamashita, H., Chiba, Y., Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Ota, T., Wakamatsu, A., Ishii, S., Yamamoto, J., Isono, Y., Kawai-Hio, Y., Saito, K., Nishikawa, T., Kimura, K., Matsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H., Kanda, K., Wagatsuma, M., Takahashi-Fujii, A., Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S., Nagahari, K., Masuho, Y., Nagai, K. and Isogai, T. NEDO human cDNA sequencing project
Unpublished
3 (bases 1 to 5347)

TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL

Isogai, T. and Yamamoto, J.
Direct Submission
Submitted (04-JUL-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7 Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan
(E-mail: genomics@hri.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986)
NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB.
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FEATURES
source

CDS

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Search completed: May 10, 2005, 00:56:06
Job time : 8949 secs

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4	2067	96.9	2094	3	CR6044596	full-length
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RESULT 2

CR626474

LOCUS

DEFINITION
full-length cDNA clone CS0E012YG17 of Placenta of Homo sapiens (human).

ACCESSION

CR626474

VERSION

CR626474.1

GI:50507281

KEYWORDS

HTC; CNSLT_cDNA.

2100 bp mRNA linear HTC 21-JUL-2004
full-length cDNA clone CS0E012YG17 of Placenta of Homo sapiens (human).
CR626474
CR626474.1
GI:50507281
HTC; CNSLT_cDNA.

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Db	1704	GGAGTGTGTC	AGCGCATCTGTCAGGGCTTCTCTCTCTGTCCTTGTGTTTGGAGAACCAAGGCT	1763
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Db	1944	TTTCTTCTA	TATTAATCAAGAGAACTTCAAGTTAATGGATGTCGGATCTCAGGCT	2003
Qy	1981	GAGAACTCG	TTCACCTCCCAAGCATTTTCATGAAAAGCTGCTTCTTATTAAATCATACAAAC	2040
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Qy	2041	TCTCACCAT	GATGTCGAAGAGTTTTCACAAATCTTTCAA 2077	
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RESULT 3				
CR605054				
LOCUS				
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ACCESSION				full-length cDNA clone CS0DI053Y021 of Placenta Cot 25-normalized
VERSION				of Homo sapiens (human).
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SOURCE	HTC; CNSLT cDNA.			
ORGANISM	Homo sapiens (human)			
REFERENCE				
AUTHORS				
TITLE				
JOURNAL				
REMARK				
REFERENCE				
AUTHORS				
TITLE				
JOURNAL				
COMMENT				
FEATURES				
source				
ORIGIN				
Query Match				
Best Local Similarity				

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Db	500	CACCTGACATACATCGGGCCCTTGCAAAATACATCCCCCTTGCTCGACTCTGAGCTGACG	559
Qy	541	GAATTCCTCCCTGCGCATGCGGGACTGGCTCAAGAAACGTCTCGTTCACCCCTGTATGAGAGG	600
Db	560	GAATTCCTCCCTGCGCATGCGGGACTGGCTCAAGAAACGTCTCGTTCACCCCTGTATGAGAGG	619
Qy	601	GATGAGGACAAACACTTCTGACTGAGAGCAGAAAGCTGCGGGTGAAGAAAGATCCATGAG	660
Db	620	GATGAGGACAAACACTTCTGACTGAGAGCAGAAAGCTGCGGGTGAAGAAAGATCCATGAG	679
Qy	661	AATGAGAAGCGCCTGGAGGACAGGAGACCAACCCTGGAGCTGCTGGGCCCGGGAATTCGAG	720
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Db	1100	CATAGATTTAAGTGAATACATTAAACGGTGTCTAAANAATGAAAATTTCTAAACCAAGACATGA	1159
Qy	1141	CATTCTTAGCTGTAACTTTAACTATTAAGGCCCTTTTCCACACGCAATTAATAGTCCCATTTT	1200
Db	1160	CATTCTTAGCTGTAACTTTAACTATTAAGGCCCTTTTCCACACGCAATTAATAGTCCCATTTT	1219
Qy	1201	TCTCTTGCCATTTGTAGCTTTGCCCATTTGCTTATTTGGCACAATGGGTGGACACGGATCTG	1260
Db	1220	TCTCTTGCCATTTGTAGCTTTGCCCATTTGCTTATTTGGCACAATGGGTGGACACGGATCTG	1279
Qy	1261	CTGGGCTCTGCTTAAACACACATTTGCAGCTTTCAACTTTCTCTTTAGTGTTCGTGTTGA	1320
Db	1280	CTGGGCTCTGCTTAAACACACATTTGCAGCTTTCAACTTTCTCTTTAGTGTTCGTGTTGA	1339
Qy	1321	AACATAACTTTACCGAGTTCAGACTTTGTGTTTCATTCTTATTCAGGCTCTTGGCTGCTGCT	1380
Db	1340	AACATAACTTTACCGAGTTCAGACTTTGTGTTTCATTCTTATTCAGGCTCTTGGCTGCTGCT	1399
Qy	1381	GGGCTTCCCCAGGTGGCCTGGAGGTGGGCAAGGAAAGTAAACAGACACACGATGTTGCTCA	1440
Db	1400	GGGCTTCCCCAGGTGGCCTGGAGGTGGGCAAGGAAAGTAAACAGACACACGATGTTGCTCA	1459
Qy	1441	AGGATGTTTTGGGACTAGAGGCTCAGTGTGGGAGAGATCCCTGCAGAAATCCACCAACC	1500
Db	1460	AGGATGTTTTGGGACTAGAGGCTCAGTGTGGGAGAGATCCCTGCAGAAATCCACCAACC	1519
Qy	1501	AGAACGTGTTTGCTCTGAGGCTGTAACTGAGAGAAAGATTTCTGGGGCTGTCTTATGAAA	1560
Db	1520	AGAACGTGTTTGCTCTGAGGCTGTAACTGAGAGAAAGATTTCTGGGGCTGTGTATGAAA	1579
Qy	1561	TATAGACATTTCTCACATAAGCCCAAGTTTCATCACCATTTCCTCTTTTACCTTTTCAAGTCAG	1620

1580	Db	TATAGACATTTCTCACAATAAGCCAGTTTCATCACATTTCTCTCTTTACCTTTTCAGTGCAG	1639
1621	Qy	TTTCTTTTTCACATTAGGCTGTGGTTCAAACCTTTTGGGACACGGACTGTCAAGTCTCTCTG	1680
1640	Db	TTTCTTTTTCACATTAGGCTGTGGTTCAAACTTTTGGGACACGGACTGTCAAGTCTCTCTG	1699
1681	Qy	GGAAATGGTTCAGCGCATCTTCGAGGGTCTCTCTCTCTCTCTCTTTTGGAGAAACAGGGCT	1740
1700	Db	GGAAATGGTTCAGCGCATCTTCGAGGGTCTCTCTCTCTCTCTCTTTTGGAGAAACAGGGCT	1759
1741	Qy	CTTCTCAGGGCTCTAGGGACTGCCAGCTGGTTTTCAGCCAGGAGGCGCAAAATCAAGAGT	1800
1760	Db	CTTCTCAGGGCTCTAGGGACTGCCAGCTGGTTTTCAGCCAGGAGGCGCAAAATCAAGAGT	1819
1801	Qy	GAGATGTAGAAAGTTGTAAATAGAAAAGTGGAGTTGGTGAATCGGTTGTCTTTCTTCCTC	1860
1820	Db	GAGATGTAGAAAGTTGTAAATAGAAAAGTGGAGTTGGTGAATCGGTTGTCTTTCTTCCTC	1879
1861	Qy	ACATTTGGATGATGTGCATAGAGTTTTTTCAGATGTTCTCTCTCTTTCTCACCTCCCTCTT	1920
1880	Db	ACATTTGGATGATGTGCATAGAGTTTTTTCAGATGTTCTCTCTCTTTCTCACCTCCCTCTT	1939
1921	Qy	TGTTCTTCTATTATATCAAGGAAACTTCAAAGTTAATGGGATGTCGGATCTTCACAGGCT	1980
1940	Db	TTTTTCTCTATTATATCAAGGAAACTTCAAAGTTAATGGGATGTCGGATCTTCACAGGCT	1999
1981	Qy	GAGAACTCGTTTCACCTCCAAAGCATTTTCATGAAAAGCTGCTTCTTATTAATCATACAAC	2040
2000	Db	GAGAACTCGTTTCACCTCCAAAGCATTTTCATGAAAAGCTGCTTCTTATTAATCATACAAC	2059
2041	Qy	TCTCACCATGATGTGAAGAGTTTCACAAATCTTTC	2075
2060	Db	TCTCACCATGATGTGAAGAGTTTCACAAATCTTTC	2094

RESULT 5	CR611642	2069 bp	mrna	linear	HTC 21-JUL-2004
LOCUS	CR611642				
DEFINITION	full-length cDNA clone CSODF007YB18 of Fetal brain of Homo sapiens (human).				
ACCESSION	CR611642				
VERSION	CR611642.1	GI:50492449			
KEYWORDS	HTC; CNSLT cDNA.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
AUTHORS	1. (bases 1 to 2069)				
TITLE	Li,W.B., Gruber,C., Jesse,J. and Polayes,D.				
JOURNAL	Full-length cDNA libraries and normalization				
REMARK	Unpublished				
	Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ Invitrogen Corporation 1500 Faraday Avenue				
REFERENCE	2. (bases 1 to 2069)				
AUTHORS	Genoscope.				
TITLE	Direct Submission				
JOURNAL	Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seque@genoscope.cns.fr				
COMMENT	- Web : www.genoscope.cns.fr) 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five primer end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. Location/Qualifiers 1. .2069 /organism="Homo sapiens" /mol_type="mrna" /db_xref="taxon:9606" /clone="CSODF007YB18" /tissue_type="Fetal brain"				
FEATURES	source				

[illegible]

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Qy	2041	TCTCACCATGATGTGAAGAGTTTCA	2065
Db	2047	TCTCACCATGATGTGAAGAGTTTCA	2071
RESULT 8			
CR592746		2068 bp	mRNA linear HTC 21-JUL-2004
LOCUS		full-length cDNA clone CS0D1002JY14 of Placenta Cot 25-normalized	
DEFINITION		of Homo sapiens (human).	
ACCESSION	CR592746		
VERSION	CR592746.1	GI:50473553	
KEYWORDS	HTC; CNSLUT_CDNA.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE			
AUTHORS	Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;		
TITLE	1 (bases 1 to 2068)		
JOURNAL	Li,W.B., Gruber,C., Jesse,J. and Polayes,D.		
REMARK	Unpublished Full-length cDNA libraries and normalization Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Faraday Avenue Genoscope. 2 (bases 1 to 2068) Direct Submission Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr) 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of invitrogen. Location/Qualifiers 1 .2068 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="CS0D1002JY14" /tissue_type="Placenta Cot 25-normalized" /plasmid="pCMVSPORT_6"		
FEATURES			
source			
ORIGIN			
Query Match	96.4%	Score 2055, 6;	DB 3; Length 2068;
Best Local Similarity	99.8%;	Pred. No. 0;	
Matches 2058;	Conservative	0;	Mismatches 4; Indels 0; Gaps 0;
Qy	1	CGGAGAGCGCGCTCTGCCTGCCGCGCTTGGCTGCGAGGCGCTTGCGAGCCCTCAGCAA	120
Db	7	CCGAGAGCGCGCTCTGCCTGCCGCGCTTGGCTGCGAGGCGCTTGCGAGCCCTCAGCAA	126
Qy	61	AGGCGCTGGATCTTCTTTCTCTTGGCTTGGCTGCGGAGGCGCTTGCGAGCCCTCAGCAA	120
Db	67	AGGCGCTGGATCTTCTTTCTCTTGGCTTGGCTGCGGAGGCGCTTGCGAGCCCTCAGCAA	126
Qy	121	GAAGCCCTGCTGATGAGACAGAGGTGGTGGAGAAAACCTGTGGCAGAGGTGACTGAGGTA	180
Db	127	GAAGCCCTGCTGATGAGACAGAGGTGGTGGAGAAAACCTGTGGCAGAGGTGACTGAGGTA	186
Qy	181	TCTGTGGGAGCTAAATCCCTGTCCAGGTGGAGTAGGAGAATTTGATGATGGTCGAGAGAA	240
Db	187	TCTGTGGGAGCTAAATCCCTGTCCAGGTGGAGTAGGAGAATTTGATGATGGTCGAGAGAA	246
Qy	241	ACCGAAGAGGAGTGGTGGCGGAAAAATCCCTGCCAGAACACCACTGCAACACGCGCAAG	300
Db	247	ACCGAAGAGGAGTGGTGGCGGAAAAATCCCTGCCAGAACACCACTGCAACACGCGCAAG	306
Qy	301	GTGTGCCAGTGGATGAGAACAAACACCCCAGATGTCGTGGTCAGGACCCCAACAGCTGC	360

307 GTGTGCGAGCTGGATGTAAGAAACAACACCCCAATGTGCGTGTGCCAGGACCCCAACAGCTGC 366
Qy
361 CCAGCCCCCAATGGCGAGTTGTGAAGGTGTGAGCAATGAGCAACAAGACCTTCGACTCT 420
Db
367 CCAGCCCCCAATGGCGAGTTGTGAAGGTGTGAGCAATGAGCAACAAGACCTTCGACTCT 426
Qy
421 TCCTGCCACTTCTTTGGCCAAAGTGCACCTCGAGGGCCAAAGAGGGCCCAAGCTC 480
Db
427 TCCTGCCACTTCTTTGGCCAAAGTGCACCTCGAGGGCCAAAGAGGGCCCAAGCTC 486
Qy
481 CACTGAGCTACATCGGGCTTGCATAATATATCCCTTGGCTTGGCTGAGCTGAC 540
Db
487 CACTGAGCTACATCGGGCTTGCATAATATATCCCTTGGCTTGGCTGAGCTGAC 546
Qy
541 GAATTCCTCCCTGGCATCGGGCTGCTCAAGAACTGCTGGTCACTCTGTATGAGAGG 600
Db
547 GAATTCCTCCCTGGCATCGGGCTGCTCAAGAACTGCTGGTCACTCTGTATGAGAGG 606
Qy
601 GATGAGGACAACACTTCTGACTGAGAAGCAGAACTGCGGGTGAAGAAGATCCATGAG 660
Db
607 GATGAGGACAACACTTCTGACTGAGAAGCAGAACTGCGGGTGAAGAAGATCCATGAG 666
Qy
661 AATGAGAGCGCTGGAGGACGAGACCAACCGTGTGAGCTGTGCGCCCGGAGCTTCGAG 720
Db
667 AATGAGAGCGCTGGAGGACGAGACCAACCGTGTGAGCTGTGCGCCCGGAGCTTCGAG 726
Qy
721 AAGAACTATAACTGTATCATCTTCCCTGTATCATCTGGCAGTTTCGGCAGCTGGACAGCAC 780
Db
727 AAGAACTATAACTGTATCATCTTCCCTGTATCATCTGGCAGTTTCGGCAGCTGGACAGCAC 786
Qy
781 CCATTTGACGGGTACCTTCTCCACACCGAGCTGGCTCCATCGGTGTCCCTCATCCCC 840
Db
787 CCATTTGACGGGTACCTTCTCCACACCGAGCTGGCTCCATCGGTGTCCCTCATCCCC 846
Qy
841 ATGAGCAATTTGACCAACCCCTTTTCGAGACCTGTGACCTGACATGACAGTATC 900
Db
847 ATGAGCAATTTGACCAACCCCTTTTCGAGACCTGTGACCTGACATGACAGTATC 906
Qy
901 GCCTGTGATGAGTGGGCGGCTGCTTCGGCATCAAGCAGAGGATATCGCAAGGATCTT 960
Db
907 GCCTGTGATGAGTGGGCGGCTGCTTCGGCATCAAGCAGAGGATATCGCAAGGATCTT 966
Qy
961 GTGATCTAAATCCACTCTTCCACAGTACCGGATCTCTTTAAACCTCCCTTCGTGT 1020
Db
967 GTGATCTAAATCCACTCTTCCACAGTACCGGATCTCTCTTTAAACCTCCCTTCGTGT 1026
Qy
1021 TTCCCTCCATGTTTAAATGTTTGGATGTTTGTCTGCTTGGGATGAGCAAGGTCGTA 1080
Db
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Qy
1081 CATGATTTTAAAGTGAATACATTAACGCTGTCTAAATGAAATTTCTAAACCAAGACATGA 1140
Db
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Qy
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Db
1147 CATTTCTAGCTGTAACCTTAACTAATTAAGGCTTTTCCACAGCATTAATAGTCCCATTTT 1206
Qy
1201 TCTCTTGCATTTGATGCTTTGGCCATTTGCTTATTTGGGACATGGGTGGACAGGATCTG 1260
Db
1207 TCTCTTGCATTTGATGCTTTGGCCATTTGCTTATTTGGGACATGGGTGGACAGGATCTG 1266
Qy
1261 CTGGGCTCTGCTTAAACACATGTCAGCTTCAACTTTTCTTTAGTGTCTGTTTGA 1320
Db
1267 CTGGGCTCTGCTTAAACACATGTCAGCTTCAACTTTTCTTTAGTGTCTGTTTGA 1326
Qy
1321 AACTAATACTTACCGAGTACAGCTTTGTGTTCATTTTCAATTCAGGGTCTTGGCTGCTGT 1380
Db
1327 AACTAATACTTACCGAGTACAGCTTTGTGTTCATTTTCAATTCAGGGTCTTGGCTGCTGT 1386
Qy
1381 GGGCTTCCCGAGTGGCTGGAGTGGGCAAGGAGTGAACACACAGATGTTGTCA 1440
Db
1387 GGGCTTCCCGAGTGGCTGGAGTGGGCAAGGAGTGAACACACAGATGTTGTCA 1446

Qy 1441 AGGATGGTGTGGAGCTAGAGGCTCAGTGTGGGAGAGATCCCTGCGAGAAATCCCAACACC 1500
Db 1447 AGGATGGTGTGGAGCTAGAGGCTCAGTGTGGGAGAGATCCCTGCGAGAAATCCCAACACC 1506
Qy 1501 AGAACGTGGTGTGGCTGAGGCTGTAACTGAGAGAAAGATTTCTGGGGCTGTCTTATGAAAA 1560
Db 1507 AGAACGTGGTGTGGCTGAGGCTGTAACTGAGAGAAAGATTTCTGGGGCTGTGTATGAAAA 1566
Qy 1561 TATAGACATTTCTCACATTAAGCCAGTTTCATCACCATTTCCTTTCACCTTTTCAGTGCGAG 1620
Db 1567 TATAGACATTTCTCACATTAAGCCAGTTTCATCACCATTTCCTTTCACCTTTTCAGTGCGAG 1626
Qy 1621 TTTCTTTTTCATATTAGGCTGTGGTTCAAACTTTTGGGAGCAGCGACTGTTCAGTTCTCTG 1680
Db 1627 TTTCTTTTTCATATTAGGCTGTGGTTCAAACTTTTGGGAGCAGCGACTGTTCAGTTCTCTG 1686
Qy 1681 GGAAGTGTGTCAGCGCATCTCTGAGGGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1740
Db 1687 GGAAGTGTGTCAGCGCATCTCTGAGGGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1746
Qy 1741 CTCTCAGGGGCTCTAGGAGCTGCCAGGCTGTTTCAGCCAGGAGGCCAAATCAAGAGT 1800
Db 1747 CTCTCAGGGGCTCTAGGAGCTGCCAGGCTGTTTCAGCCAGGAGGCCAAATCAAGAGT 1806
Qy 1801 GAGATGTAGAAAAGTTGTAAAATAGAAAAGTGGAGTTGGTGAATCGGTTGTTCTTCTCTC 1860
Db 1807 GAGATGTAGAAAAGTTGTAAAATAGAAAAGTGGAGTTGGTGAATCGGTTGTTCTTCTCTC 1866
Qy 1861 ACATTTGGATGATGTGCATTAAGGTTTTTATAGCTGTTCTCTCTCTCTCTCTCTCTCTCTCT 1920
Db 1867 ACATTTGGATGATGTGCATTAAGGTTTTTATAGCTGTTCTCTCTCTCTCTCTCTCTCTCTCT 1926
Qy 1921 TGTCTCTTCTTATTAATCAAGAGAACTTCAAGTTAAATGGATGTCGATGTCGATGTCACAGCT 1980
Db 1927 TTTTCTTCTTATTAATCAAGAGAACTTCAAGTTAAATGGATGTCGATGTCGATGTCACAGCT 1986
Qy 1981 GAGAACTCGTTTCACTCCAGCAATTTTCATGAAAAGCTGCTTCTTATTAATCATACAAC 2040
Db 1987 GAGAACTCGTTTCACTCCAGCAATTTTCATGAAAAGCTGCTTCTTATTAATCATACAAC 2046
Qy 2041 TCTCACCATGATGTGAAGATT 2062
Db 2047 TCTCACCATGATGTGAAGATT 2068

RESULT 9
CR604100
LOCUS
DEFINITION
full-length cDNA clone CS0DB011VH01 of Placenta of Homo sapiens (human)
ACCESSION
CR604100
VERSION
CR604100.1
KEYWORDS
HTC; CNSLT_cDNA.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 2071)
Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
REMARK
Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue
2 (bases 1 to 2071)
REFERENCE
CR604100
AUTHORS
TITLE
JOURNAL
COMMENT
Submitted (20-JUL-2004) Genoscope - Centre National de Sequenage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
- Web : www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned

QY	781	CCCATTGACGGGTACCTCTCTCCACACACCGAGCTGGCTCACTGCGTGTCTCCCTCATCCCC	840
DB	803	CCCATTGACGGGTACCTCTCTCCACACACCGAGCTGGCTCCACTGCGTGTCTCCCTCATCCCC	862
QY	841	ATGAGCAATTGCACCAACCGCTTTTTCGAGACCTGTGTACCTTGGACAAATGACAAGTACATC	900
DB	863	ATGAGCAATTGACACCAACCGCTTTTTCGAGACCTGTGTACCTTGGACAAATGACAAGTACATC	922
QY	901	GCCCTGGATGAGTGGCGCGGCTGTTTCCGCAATCAAGCAGAAAGGATATCGACAAGGATCTT	960
DB	923	GCCCTGGATGAGTGGCGCGGCTGTTTCCGCAATCAAGCAGAAAGGATATCGACAAGGATCTT	982
QY	961	GTGATCTAAATCCACTCCTTCCACAGTACCGGATTTCTCTTTTAAACCTTCCCTTCGTGT	1020
DB	983	GTGATCTAAATCCACTCCTTCCACAGTACCGGATTTCTCTCTTTTAAACCTTCCCTTCGTGT	1042
QY	1021	TTCCCCCAATGTTTAAATGTTTGGATGTTTGTGTGTTCTGCCCTGGAGACAAGGTGCTAA	1080
DB	1043	TTCCCCCAATGTTTAAATGTTTGGATGTTTGTGTGTTCTGCCCTGGAGACAAGGTGCTAA	1102
QY	1081	CATAGATTTAAGTGAATACATTAACGGTGTCTAAATAAGAAATTTCTAAACCAAGCATGA	1140
DB	1103	CATAGATTTAAGTGAATACATTAACGGTGTCTAAATAAGAAATTTCTAAACCAAGCATGA	1162
QY	1141	CATTCTTAGCTGAACCTTAACCTATTAAGGCTCTTTTCCACAGCATTAATAGTCCCATTTT	1200
DB	1163	CATTCTTAGCTGAACCTTAACCTATTAAGGCTCTTTTCCACAGCATTAATAGTCCCATTTT	1222
QY	1201	TCTCTTGCCATTGTTAGCTTTGGCCATTGTCTTATTTGGCACAATGGGTGGACACGGATCTG	1260
DB	1223	TCTCTTGCCATTGTTAGCTTTGGCCATTGTCTTATTTGGCACAATGGGTGGACACGGATCTG	1282
QY	1261	CTGGGCTCTGCTTAAACACACATGTCAGCTTCAACTTTTCTCTTTAGTGTCTGTTTGA	1320
DB	1283	CTGGGCTCTGCTTAAACACACATGTCAGCTTCAACTTTTCTCTTTAGTGTCTGTTTGA	1342
QY	1321	AACATAATCTTACCGAGTCAGACTTTGTGTTTCAATTTTCAAGGTCCTTTGGCTGCCGT	1380
DB	1343	AACATAATCTTACCGAGTCAGACTTTGTGTTTCAATTTTCAAGGTCCTTTGGCTGCCGT	1402
QY	1381	GGGCTTCCCCAGGTGGCTGTGAGGTGGGCAAGGGAAGTAAACACACACGATGTTCTCA	1440
DB	1403	GGGCTTCCCCAGGTGGCTGTGAGGTGGGCAAGGGAAGTAAACACACACGATGTTCTCA	1462
QY	1441	AGGATGTTTTGGGACTAGAGGCTCAGTGTGGAGAGATCCCTCGAGAAATCCACCAACC	1500
DB	1463	AGGATGTTTTGGGACTAGAGGCTCAGTGTGGAGAGATCCCTCGAGAAATCCACCAACC	1522
QY	1501	AGAACGTGTTTTGCTCAGGCTGTAACTGAGAGAAAGATTTCTGGGGCTGTCTTATGAAA	1560
DB	1523	AGAACGTGTTTTGCTCAGGCTGTAACTGAGAGAAAGATTTCTGGGGCTGTCTTATGAAA	1582
QY	1561	TATAGACATTCTCACAATAGCCCCAGTTTCATCACCATTTTCTCTCTTTACCTTTTCA	1620
DB	1583	TATAGACATTCTCACAATAGCCCCAGTTTCATCACCATTTTCTCTCTTTTCA	1642
QY	1621	TTTCTTTTTCATTTAGGCTGTGTTTCAACTTTTGGAGGACACGACTGTCTCTG	1680
DB	1643	TTTCTTTTTCATTTAGGCTGTGTTTCAAACTTTTGGGAGCAGGACTGTCTCTCTG	1702
QY	1681	GGAAGTGGTCAGCGCATCTCGAGGGCTTCTCTCTCTCTGTCCTTTTGGAGAACACGGCT	1740
DB	1703	GGAAGTGGTCAGCGCATCTCGAGGGCTTCTCTCTCTCTGTCCTTTTGGAGAACACGGCT	1762
QY	1741	CTTCTCAGGGCTCTTAGGACTCGCAGGCTGTTTTCAGCCAGGAAGGCCAAATCAAGAGT	1800
DB	1763	CTTCTCAGGGCTCTTAGGACTCGCAGGCTGTTTTCAGCCAGGAAGGCCAAATCAAGAGT	1822
QY	1801	GAGATGTAGAAAGTTGTAAATAAGAAAAAGTGGAGTTGGTGAATCGGTTGTTCTTCTCCTC	1860
DB	1823	GAGATGTAGAAAGTTGTAAATAAGAAAAAGTGGAGTTGGTGAATCGGTTGTTCTTCTCCTC	1882

Qy	1861	ACATTGGATGATGTGCATGAAGGTTTTTACATGTTTCCTCCTTTCTTCAACCTCCGCCCTT	1921
Db	1883	ACATTGGATGATGTGCATGAAGGTTTTTACATGTTTCCTCCTTTCTTCAACCTCCGCCCTT	1942
Qy	1921	TGTTCTTCTTAATTAATCAAGAAGAACTTCAAGTTAATGGGATCGTGCGATCTCACAGGCT	1980
Db	1943	TTTCTTCTTAATTAATCAAGAAGAACTTCAAGTTAATGGGATCGTGCGATCTCACAGGCT	2002
Qy	1981	GAGAACTCGTTACCTCCAAGCATTTTCATGAAAAAGCTGCTTCTTATTATCATACAAC	2040
Db	2003	GAGAACTCGTTACCTCCAAGCATTTTCATGAAAAAGCTGCTTCTTATTATCATACAAC	2062
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Db	2063	TCTCACCATCATGTGAAGA	2081
RESULT	12		
CR622084			
LOCUS	CR622084	2063 bp mRNA linear HTC 21-JUL-2004	
DEFINITION	full-length cDNA clone CS0DE001YB16 of Placenta of Homo sapiens (human).		
ACCESSION	CR622084		
VERSION	GI:50502891		
KEYWORDS	HTC; CNSLT_cDNA.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	Li, W.B., Gruber, C., Jessee, J. and Polayes, D.		
TITLE	Full-length cDNA libraries and normalization		
JOURNAL	Unpublished		
REMARK	Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ InvitroGen Corporation 1600 Paraday Avenue 2 (bases 1 to 2063) Genoscope. Direct Submission Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - web : www.genoscope.cns.fr) 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.		
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
COMMENT			
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	/mol_type="mRNA"		
	/db_xref="taxon:9606"		
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	/tissue_type="Placenta"		
	/plasmid="pCMVSPORT_6"		
ORIGIN			
Query Match	96.1%; Score 2050.6; DB 3; Length 2063;		
Best Local Similarity	99.8%; Pred. No. 0;		
Matches 2053; Conservative	0; Mismatches 4; Indels 0; Gaps 0;		
Qy	1	CGGAGAGGCGGCTCTGCGCTCGCGCTGCTGCCTGCACCTGAGGGTCCCAGCACCATG	60
Db	7	CCGAGAGGCGGCTCTGCGCTCGCGCTGCTGCCTGCACCTGAGGGTCCCAGCACCATG	66
Qy	61	AGGCGCTGGATCTTCTTTCTTCCTTTGCTGGCGGGAGGGCCCTTGGCAGCCCCCTCAGCAA	120
Db	67	AGGCGCTGGATCTTCTTTCTTCCTTTGCTGGCGGGAGGGCCCTTGGCAGCCCCCTCAGCAA	126
Qy	121	GAAGCCCTGCCTGATCAGACAGAGGTGGTGGAGAATACTGTGGCAGAGGTGACTGAGGTA	180
Db	127	GAAGCCCTGCCTGATCAGACAGAGGTGGTGGAGAATACTGTGGCAGAGGTGACTGAGGTA	186

QY 181 TCTGTGGAGCTAATCTCTGTCCAGGTGGAAGTAGAGAAATTGTATGATGGTGCAGAGGAA 240
DB 187 TCTGTGGAGCTAATCTCTGTCCAGGTGGAAGTAGAGAAATTGTATGATGGTGCAGAGGAA 246
QY 241 ACCGAGAGGAGGTGGTGGCGGAAATCCCTGCCAGAACCCACCACTGCAACACCGGCAAG 300
DB 247 ACCGAGAGGAGGTGGTGGCGGAAATCCCTGCCAGAACCCACCACTGCAACACCGGCAAG 306
QY 301 GTGTCCGAGCTGGATGAGAAACAAACCCCAATGTGCTGTGCGAGGACCCCAACAGCTGC 360
DB 307 GTGTCCGAGCTGGATGAGAAACAAACCCCAATGTGCTGTGCGAGGACCCCAACAGCTGC 366
QY 361 CCAGCCCCAATTTGGCGAGTTTGAGAGGTGTGAGCAATGACAAACCACTTTCGACTCT 420
DB 367 CCAGCCCCAATTTGGCGAGTTTGAGAGGTGTGAGCAATGACAAACCACTTTCGACTCT 426
QY 421 TCCTGCCACTTCTTTGCCACAAGTGCACCTGGAGGGCACCAAGAGGGCCACAAGCTC 480
DB 427 TCCTGCCACTTCTTTGCCACAAGTGCACCTGGAGGGCACCAAGAGGGCCACAAGCTC 486
QY 481 CACCTGGACTACATCGGGCTTTGCAATATACATCCCTTGCCTGGACTCTGAGCTGACC 540
DB 487 CACCTGGACTACATCGGGCTTTGCAATATACATCCCTTGCCTGGACTCTGAGCTGACC 546
QY 541 GAATTCCTCCCTGCGCATGCGGAGCTGGCTCAAGAACTGCTCTGGTCACTCTGTATGAGAG 600
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DB 667 AATGAGAGCGCTCGAGGAGGAGACCAACCCCTGAGAGCTGCTGCGCCGGGACTTCGAG 726
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QY 1801 GAGATGTAGAAAGTTGTAAATAGAAAAGTGGAGTCTGGTGAATCGGTTGTTCTTTCTCTC 1860
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QY 1861 ACATTTGGATGATGTCTATAAGTTTTTATGATGTTTCTCTCTCTCTCTCTCTCTCTCTCTCT 1920
DB 1867 ACATTTGGATGATGTCTATAAGTTTTTATGATGTTTCTCTCTCTCTCTCTCTCTCTCTCTCT 1926
QY 1921 TGTCTCTTATTAATCAAGAGAACTTCAAGTTAATGGATTAATGGATGTCGATCTCACAGGCT 1980
DB 1927 TTTTCTCTTATTAATCAAGAGAACTTCAAGTTAATGGATTAATGGATGTCGATCTCACAGGCT 1986
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DB 1987 GAGAACTCGTTTCACTCCCAAGCATTTTCATGAAAAAGCTGCTTCTTATTAATCATACAAAC 2046
QY 2041 TCTCACCATGATGTGAA 2057
DB 2047 TCTCACCATGATGTGAA 2063

RESULT 13

CR613247

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REMARK

CR613247 2080 bp mRNA linear HTC 21-JUL-2004
full-length cDNA clone CS0DE014YJ02 of Placenta of Homo sapiens
(human).
CR613247 GI:50494054
HTC; CNSLT_cDNA.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
Contact : Feng Liang Email : fliang@lifetech.com URL :


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Db 1824 GAGATGTAGAAAGTTGTAAATAGAAAAGTGGAGTGGTGAATCGGTGTTCTTTCTC 1883
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QY 1861 ACATTGGATGATTCATCAAGGTTTATAGCATGTTCTCCCTTTCTTCACCCCTCCCTT 1920
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Db 1884 ACATTGGATGATTCATCAAGGTTTATAGCATGTTCTCCCTTTCTTCACCCCTCCCTT 1943
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Db 2064 TCTCACCATGATGTGAA 2080
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RESULT 14
CR612102
LOCUS
DEFINITION
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sapiens (human).
ACCESSION
CR612102
VERSION
CR612102.1 GI:50492909
KEYWORDS
HTC; CNSLT_CDNA.
SOURCE
Homo sapiens
ORGANISM
Homo sapiens
REFERENCE
1 (bases 1 to 2040)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS
Li W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE
Full-length cDNA libraries and normalization
JOURNAL
Unpublished
REMARK
Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Paraday Avenue
2 (bases 1 to 2040)
Genoscope.
REFERENCE
Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
Bp 191 91006 EVRY cedex - FRANCE [E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr]
COMMENT
1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
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/clone="CS0DA011YE02"
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Best Local Similarity 99.8%; Pred. NO. 0;
Matches 2036; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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|||||
QY 103 TTGGCAGCCCTCAGCAAGAACCCCTGCTGTATGAGACAGAGTGGTGGAGAAACTGTG 162
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Db 1021 CTGGAGACAAAGGTGCTTAACATAGATTTAGTGAATACATTAACGGTGTCAAAAATCAAAA 1080
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QY 1183 CATTAAATAGTCCCATTTTCTCTTGGCATTTGTAGCTTTGGCCATTTGCTTATTGGCACA 1242
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Db 1201 TGGGTGACACGGATCTGCTGGCTCTGCCCTTAACACACATTCAGCTTCAACTTTCT 1260
Qy 1303 CTTTGTAGTCTCTGTTTGAACCTAATCTACCGAGTCTGAGCTTGTGTTTCATTTTC 1362
Db 1361 CTTTGTAGTCTCTGTTTGAACCTAATCTACCGAGTCTGAGCTTGTGTTTCATTTTC 1320
Qy 1363 AGGCTCTTGGCTGCTGCTGGGCTTTCCCGAGTCTGAGGCTGGGCAAGGGAAGTAAC 1422
Db 1321 AGGCTCTTGGCTGCTGCTGGGCTTTCCCGAGTCTGAGGCTGGGCAAGGGAAGTAAC 1380
Qy 1423 AGACACACGATGTTGTCAAGATGTTTGGGACTAGAGGCTCAGTGTGGGAGAGATCC 1482
Db 1381 AGACACACGATGTTGTCAAGATGTTTGGGACTAGAGGCTCAGTGTGGGAGAGATCC 1440
Qy 1483 CTGCAGATCCACCAACGAGACCTGTTTGGCTGAGGCTGTACTGAGAGAGATCTT 1542
Db 1441 CTGCAGAACCCCAACGAGACCTGTTTGGCTGAGGCTGTACTGAGAGAGATCTT 1500
Qy 1543 GGGGCTCTCTTATGAAATATAGACATCTCACATAAGCCAGTTCATCACCATTTCTCTC 1602
Db 1501 GGGGCTCTGTATGAAATATAGACATCTCACATAAGCCAGTTCATCACCATTTCTCTC 1560
Qy 1603 CTTTACCTTTCAGTGCAGTTCTTTTTCATATAGGCTGTGGTTCATAAATTTTGGGAC 1662
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Qy 1903 TTTCTTCACTCTCCCT 1962
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Qy 2023 CTTTATTAATCATCAAACTCTCACCATGATGTGAGAGTTTCATAAATCTTCAAAATAA 2082
Db 1981 CTTTATTAATCATCAAACTCTCACCATGATGTGAGAGTTTCATAAATCTTCAAAATAA 2040

RESULT 15
LOCUS CR625661
DEFINITION full-length cDNA clone CS0DA011YN21 of Neuroblastoma of Homo sapiens (human).
ACCESSION CR625661
VERSION CR625661.1 GI:50506468
KEYWORDS HTC; CNSLT_cDNA.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2038)
AUTHORS Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished

REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Paraday Avenue
2 (bases 1 to 2038)
Genoscope.
Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seque@genoscope.cns.fr)
- Web : www.genoscope.cns.fr)
COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
FEATURES
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/plasmid="pCMVSPORT_6"
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Best Local Similarity 99.8%; Pred. No. 0;
Matches 2034; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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Db 61 TTGCGAGCCCTCAGCAAGAACCCCTCCCTGATGACAGAGTGTGGAGAACTGTG 120
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Qy 283 CACTGCAAAACACGCGAAGGTGCGAGCTGATGAGAAACACACCCCATGTGGTGTGC 342
Db 241 CACTGCAAAACACGCGAAGGTGCGAGCTGATGAGAAACACACCCCATGTGGTGTGC 300
Qy 343 CAGGACCCCAACAGCTGCCAGCCCTCATTTGGCGAGTTTTCAGAGGTGTGCGACCAATGC 402
Db 301 CAGGACCCCAACAGCTGCCAGCCCTCATTTGGCGAGTTTTCAGAGGTGTGCGACCAATGC 360
Qy 403 AACAGACCTTCAGTCT 462
Db 361 AACAGACCTTCAGTCT 420
Qy 463 AAGAAGGCCACAAAGCTCCACCTGGACTACATCGGCGCTTGCATAATATATCCCTCTTC 522
Db 421 AAGAAGGCCACAAAGCTCCACCTGGACTACATCGGCGCTTGCATAATATATCCCTCTTC 480
Qy 523 CTGGACTCTGAGCTGACCGAATTTCCCTCTGCGATGCGGACTGGCTCAAGAAAGCTCTG 582
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Db 661 |||||CGGCCCGGAGCTTCGAGAAGAACTATATACATGTACATCTTCCCTGTACACTGGCAGTTC 720
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Qy 823 CGTGTCTCCCTCATCCCATNGAGAGATTGACACACCGCTTTTTCGAGACCTGTGACCTG 882
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Qy 943 GATATCGACAAGGATCTTGTGATCTAAATCCACTCTCTCCACAGTACCGGATTTCTCTTT 1002
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Search completed: May 10, 2005, 02:40:37
Job time : 6268 secs

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Db 1801 ATCGGTTGTTCTTCTTCTCCTCACATTTGGATGATTGTCAFAAGGTTTTCATGATGTTCTCTCT 1860
Qy 1903 TTTCTTCACCCCTCCCTTTGTTCTTCTTATTAATCAAGAGAAACTTCAAAAGTTAAATGGGAT 1962
Db 1861 TTTCTTCACCCCTCCCTTTTCTTCTTATTAATCAAGAGAAACTTCAAAAGTTAAATGGGAT 1920
Qy 1963 GGTCCGATCTCACAGGCTGAGAACTCGTTACCTTCAAGCATTTTCATGAAAAAGCTGCTT 2022
Db 1921 GGTCCGATCTCACAGGCTGAGAACTCGTTACCTTCAAGCATTTTCATGAAAAAGCTGCTT 1980
Qy 2023 CTTATTAATCATACAAACTCTCACCATGATGTGAAGAGTTTCACAAATCTTTCAAAAT 2080
Db 1981 CTTATTAATCATACAAACTCTCACCATGATGTGAAGAGTTTCACAAATCTTTCAAAAT 2038